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Search information block:
Query: US-09-030-606-111
Query length: 1289
Database: PIR_60:*
Database sequences: 122810
Database length: 40055486
Search time (sec): 182.540000
                                                    Pir1: S39262
pir1: S45511
pir2: I45589
pir1: A40181
pir1: A40229
pir1: A42929
pir2: I46080
pir2: I47141
pir2: S44611
pir2: S44611
pir2: S55345
pir2: J00317
pir2: J00317
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pir1:JC2297
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pir1:139368
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pir1:A46472
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-q-/cgn2_1/USPT0_spco1/US09030606/runat_24091999_171617_29825/app_query.fasta.1
-DB-PIR_60 -QFMT-fastan -SUFFIX-rpr -GAPOP-12.000 -GAPEXT-4.000
-MINNATCH-0.100 -LOOPEL-0.000 -LOOPEXT-0.000 -GAPOP-6.000
-QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cd1
-LIST-45 -DOCALIGN-200 -THR_SCORE-escore -ALIGN-15 -MODE-LOCAL
-OUTFMT-pfs -NORM-stat -USER-US09030606 -NCPU-6 -ICPU-3 -WAIT
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gastric mucin (clone PGM-2A) -
CO2F5.8 protein - Caenorhabditi
cobalamin biosynthesis protein
probable membrane protein YCRC
mucin 6, gastric (3-repeat clon
hypothetical 82K protein - Xant
development-specific membrane p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Cell surface protein TAPA-1 - CD63 antigen - rabbit CD9 antigen - bovine | CD63/ME491 antigen homolog - Cell surface protein TAPA-1 - CD9 antigen - rat CD9 antigen - rat CD63/ME491 antigen homolog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l antigen - mouse
1 23K integral mem
1 CD9 antigen - hu
1 CD9 antigen - gr
glucan 1,4-alpha-glucosidase retinal degeneration slow protwith Wilms' tumor protein WT1 - rat histidine rich calcium binding Wilms tumor susceptibility pro
                                                                                                                        mucin (clone PGM-2B) - pig
Wilms' tumor protein analog, W7
TYL protein - human
1 MSB2 protein - yeast (Saccharchypothetical 66K protein - Onor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell acute lymphoblastic leuk
tumor-associated antigen CO-029
cell surface glycoprotein CD37
hemopoletic cell surface glycop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD9 antigen - human
CD9 antigen - green monkey
uroplakin Ia - bovine
uroplakin Ib - bovine
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C33/R2/IA4 - mouse
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US-09-030-606-111 x B47629
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A; Residues: 1-281 <CLA>
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pir1:PNLJCN
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Percent Similarity:
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                                                 LeuPheAlaThrGlnIleThrLeuGlyIleLeuIleSerThrGlnArgVa
                                                                                                ATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCAC
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Length: 286 Gaps: 7 Percent Identity: 28.322

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cell surface glycoprotein cur, ___ CN; Alternate names: leukocyte antigen CD37
N;Alternate names: leukocyte antigen CD37
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 09-Aug-1996 #text_change 05-Sep-1997
C;Date: 1-- PA78700. TC1501
F:13-38/Domain: transmembrane #status predicted <TM1>
F:39-59/Domain: extracellular #status predicted <EX1>
F:60-80/Domain: transmembrane #status predicted <TM2>
F:81-85/Domain: htracellular #status predicted <CY2>
F:86-110/Domain: transmembrane #status predicted <CY3>
F:111-241/Domain: extracellular #status predicted <EX2>
F:211-242-267/Domain: transmembrane #status predicted <EX2>
F:268-278/Domain: intracellular #status predicted <TM4>
F:268-278/Domain: intracellular #status predicted <CY3>
F:170,183,188/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: B47629; JCÍ501

R;Classon, B.J.; Williams, A.F.; Willis, A.C.; Seed, B.; Stamenkovic, J. Exp. Med. 172, 1007, 1990
A;Reference number: A47629
A;Accession: B47629
                                                                                                                                                                                                                                                    C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lymphocyte; transmembrane
F;2-12/Domain: intracellular #status predicted <CYI)
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X53517; NID:g55911; PID:g55912
C;Comment: This antigen is expressed abundantly on B lymphocytes
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! laminin beta-1 chain precur
        #status predicted
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C:Species: Homo sapiens (man)
C:Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 20-Mar-1998
C:Accession: 138942; S16156; A46493
R:Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Science 268, 884-886, 1995
A:Title: KAII, a metastasis suppressor gene for prostate cancer on human chrome A:Reference number: 138942; MUID:95273964
A:Accession: 138942
A:Cross-references: EMBL:X53795; NID:g35832; PID:g35833
A;NOte: the authors translated the codon ACC for residue 50 as Thr
R;Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukul
J. Immunol. 149, 2879-2886, 1992
A:Title: C33 antigen recognized by monoclonal antibodies inhibitor:
                                                                                                                                                                                                  A;Cross-references: EMBL:U20770; NID:g806805; PID:g806806
R;Gaugitsch, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.
Eur. J. Immunol. 21, 377-383, 1991
A;Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homolog A;Reference number: S16156; MUID:91153380
A;Accession: S16156
                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-267 <GAU>
                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-267 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: cell surface glycoprotein KAI1; membrane protein R2, inducible;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastasis suppressor KAI1 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: pirl:A46493
                                                                                                                                                                                Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162
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rLeuSerIlePheLeuCysArgAsnLeuAspHisValTyrAspArgLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysSerCysTyrAsnSerThrAlaThrAsnAspSerSerGlyPheAspLys 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nLysAlaGlnMetLeuLysAlaAsnGlySerGluGluLeuPheValProC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTATGGTTCCCAGGAAGACTTCACT.....CAAGTGTGGAACACC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laArgTyr 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCACTAC 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGTCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luGlyCysAlaArgSerLeuGlnLysTrpLeuHisAsnAsnIleIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGGTTGCTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nThrAlaAspIleCysAlaLeuProAlaLysAlaHisIleTyrArg...G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuPheLeuSerGlnLeuSerArgLeuGlyProArgAlaLysLeuArgGl 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACTCACCCTACTTCAAAGAGAACAGTGCC.....TTTCCCC 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCATGAAAGGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erTyrArgThrAsnProAspGluThrAlaAlaGluGluSerTrpAspTyr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . ACAGCCAATGAAACCTGCACCAAGCAAAAGGCTCACGACCAAAAAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
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       inhibitory to
                                                                                                                                                                                                                                                                                                                                                                                                          GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
                                                     Fukuhara,
          human T
                                                        N.; Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isaacs,
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          Leuk
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A; Map position: 11p11.2-11p11.2

C; Superfamily: CD9 antigen

C; Keywords: glycoprotein; transmembrane protein

E; 1-10/Domain: intracellular *status predicted <CY1>
E; 11-36/Domain: transmembrane *status predicted <TM1>
E; 37-57/Domain: transmembrane *status predicted <TM2>
E; 38-78/Domain: transmembrane *status predicted <CY2>
E; 58-78/Domain: intracellular *status predicted <CY2>
E; 44-108/Domain: transmembrane *status predicted <TM3>
E; 28-25/Domain: extracellular *status predicted <TM3>
E; 28-25/Domain: transmembrane *status predicted <CY3>
E; 28-25/Domain: attransmembrane *status predicted <CY3>
E; 28-25/Domain: intracellular *status predicted <CY3>
E; 28-25/Domain: intracellular *status predicted <CY3>
E; 29-25/Domain: intracellular *status predicted <CY3>
E; 29-
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A; Reference number: A46493; MUID:93017900
A; Accession: A46493
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-239', MV', 242-267 <IMA>
A; Cross-references: GB:S48196; NID:9258294; PID:9258295
A; Experimental source: T-cell line MOLT-4
A; Note: seguence extracted from NCBI backbone (NCBIP:117
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-030-606-111 x A46493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: KAI1
A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: A46493 from:
                                                                            520 AGGAAGACTTCACTCAA...GTGTGGAACACCACCATGAAAGGGCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 TCTGTGTGGGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT
                                                                                                                                                                      115 nGluMetGlyGlyIleValThrGluLeuIleArgAspTyrAsnSerSerA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 GCAGCTGCTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 CCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTGAGGTT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 TGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 TTTGTCAACGTGGGC...TACTTCCTCATCGCAGCCGGCGTTGTGGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 GGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 tLeuMetGlyPheLeuGlyCysIleGlyAlaValAsnGluValArgCysL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 ysSerSerPheIleSerValLeuGlnThrSerSerSerSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 eIleLeuGlyAlaValIleLeuGlyPheGlyValTrpIleLeuAlaAspL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 euLeuGlyLeuTyrPheAlaPheLeuLeuLeuIleLeuIleAlaGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 CysIleLysValThrLysTyrPheLeuPheLeuPheAsnLeuIlePhePh
rgGluAspSerLeuGlnAspAlaTrpAspTyrValGlnAlaGlnValLys
                                                                                                                                                                                                                                                                 GACGTTG...CTGGTAGTGCCTGCCATCAAGAAAGATTAT...GGTTCCC
                                                                                                                                                                                                                                                                                                                                                           ThrAlaGly.....AlaLeuPheTyrPheAsnMetGlyLysLeuLysGl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...LeuArgMetGlyAlaTyrValPheIleGlyValGlyAlaValThrMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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1.763
62.313
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Gaps:
Percent Identity:
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6
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11
29.851
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148
                                                                                     566
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                                                                                                                                                                                                                                                                          519
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seq_documentation_block:
C33/R2/IA4 - mouse
C33/R2/IA4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Feb-1997
C;Accession: I49561
R;Nagira, M.; Imai, T.; Ishikawa, I.; Uwabe, K.I.; Yoshie, O.
Cell. Immunol. 157, 144-157, 1994
A;Title: Mouse homologue of C33 antigen (CD82), a member of the transmembrane 4 superfam A; Reference number: I49561; MUID:94313678
A;Accession: I49561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-400 <rbox
A;Cross-references: GB:D14883; NID:g984036; PID:g498368
C:Superfamily: CD9 antigen
                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-030-606-111 x I49561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-266 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: pir2:I49561
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: I49561 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 euGlyValGlyValGlyValAlaIleIleGluLeuGlyMetValLeu 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 tAsnArgProGluValThrTyrProCysSerCysGluValLysGlyGluG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    567 TGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTC.. 614
                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     869 CTAC 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       819 TCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCTGCCA 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         769 GIGGIGIGGAGCIGGAAIIGGGGGCCICGAGCIGGCIGCCAIGAIIGIG 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 yCysMetGluLysValGlnAlaTrpLeuGlnGluAsnLeuGlyIleIleL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719 TTGCTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGTCACCGTGG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 ArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGl 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 luAspAsnSerLeuSerValArgLysGlyPheCysGluAlaProGlyAsn 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615 ....AAAGAGAACAGTGCCTTTCCCCCATTCTGT......TGCA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 CysCysGlyTrpValSerPheTyrAsnTrpThrAspAsnAlaGluLeuMe 165
                                                  229 GGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAG 278
                                                                                                                                                                                                                                                  129 TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 gHis 255
                                                                                               38
                                                                                                                                                                                                   TCTGTGTGCGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG 228
  ysAsnSerPheIleSerValLeuGlnThrSerSerSerSer......
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                                                                                                                                                                                                                                                                                                                                                                                                                                 284.00
1.753
58.273
                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 278
Gaps: 10
Percent Identity: 28.058
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6
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                                                                                                                                                                                                      21
51
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	: pir1:139368	q_name
		250
	TCTACAATAAGTCCACTTCTGCCTCTGCCACTAC 872	839
249	alaValIleGluLeuLeuGlyLeuPheLeuSerIle	238
237		221
788	ATGACATCCGAACTAATGCAGTCACCGTGGGTGGTGGTGGCAGCTGGAATT 7	739
221	nProGluAspTrpProValAsnThrGluGlyCysMetGluLysAlaGlnA	204
738	-	695
204	ValLysLysGlyPheCysGluAlaAspAsnSerThrValSerGluAsnAs	188
694		645
187	hrTyrProCysSerCysGluLysIleLysGluGluAspAsnGlnLeuIle l	171
644	TTCCCCCATTCTGT	628
171	STyrAsnTrpThrGluAsnGluGluLeuMetGlyPheThrLysThrT 1	155
627		582
155	AlaTrpAspTyrValGlnAlaGlnValLysCysCysGlyTrpValSerHi 1	139
581	:	537
138	etAspIleIleArgAsnTyrThrAlaAsnAlaThrSerSerArgGluGlu]	122
536	CAA	522
122	uPheTyrPheAsnAlaAspLysLeuLysLysGluMetGlyAsnThrValM 1	105
521		476
105	ThrValGlyValLe]	101
475		426
100	euLeuGlyLeuTyrPheValPheLeuLeuIleLeuIleAlaGlnVal 1	84
425		376
84	ysL	67
375		326
67	LeuGlnValGlyAlaTyrValPheileGlyValGlyAlaIleThrIl 6	52
325		279

R:Emi, N.; Kitaori, K.; Seto, M.; Ueda, R.; Saito, H.; Takahashi, T. Immunogenetics 37, 193-198, 1993
A;Title: Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 supe A;Reference number: I39368; MUID:93131291
A;Accession: I39368 T-cell acute lymphoblastic leukemia associated antigen 1 - human N;Alternate names: cell surface glycoprotein (clone Al5); TALLA-1 C;Species: Homo sapiens (man) C;Date: 23-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 13-Sep-1997 C;Accession: I3958; I54784 A; Molecule type: mRNA A; Residues: 1-244 < RES> A;Cross-references: GB:D10653; NID:g285900; PID:g285901 A;Experimental source: immature T cell line HPB-ALL seq_documentation_block:

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A, Map position: Xq11-Xq11
C; Superfamily: CD9 antigen
C; Keywords: glycoprotein; surface antigen; transmembrane prote; l-11/Domain: intracellular #status predicted <CY1>
F; 12-35/Domain: transmembrane #status predicted <EM1>
F; 36-51/Domain: transmembrane #status predicted <CM2>
F; 77-80/Domain: transmembrane #status predicted <CY2>
F; 77-80/Domain: transmembrane #status predicted <CY2>
F; 81-102/Domain: transmembrane #status predicted <CM3>
F; 103-207/Domain: transmembrane #status predicted <CM3>
F; 208-232/Domain: transmembrane #status predicted <CY3>
F; 208-232/Domain: intracellular #status predicted <CY3>
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us-09-030-606-111 x 139368
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A;Molecule type: mRNA
A;Residues: 1-244 <RE2>
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A;Title: Identification of the specific surface marker of T-cell acute lymphoblasti A;Reference number: 154784; MUID:95286314
A;Accession: 154784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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A;Cross-references: GDB:202921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 ACCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 GCTCATCTTTCTGTGGGGCAGCCCTGTTGGCAGTGGGCATCTGGGTGT 219
                                                                 520 AGGAAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGC 569
                                                                                                                                  113 pThrPheLeuArgThrTyrThrAspAlaMet...GlnThrTyrAsnGlyA 129
                                                                                                                                                                                                                                                                                                                                 420 GAGGTTGCAGCTGCTGGTCGCCTTGGTGTACACCACAATGGCTGAGCA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 GCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ThrLysProValIleThrCysLeuLysThrLeuLeuIleIleTyrSerPh
                                                                                                                                                                                                                                                             rIleValValPheGlyLeuPheGlyCysPheAlaThrCysArgGlySerP
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                                                                                                                                                                                               CTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAAAGATTATGGTTCCC 519
                                                                                                                                                                                                                                                                                                                                                                                               roTrpMetLeuLysLeuTyrAlaMetPheLeuSerLeuValPheLeuAla 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCTTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCA 369
snAspGluArgSerArgAlaValAspHisValGlnArgSerLeuSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCT 419
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1.775
64.490
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Gaps:
Percent Identity:
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6
26.939
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C;Accession: A36056

R;Szala, S.; Kasal, Y.; Steplewski, Z.; Rodeck, U.; Koprowski, H.; Linnenbach, A.J. Proc. Natl. Acad. Sci. U.S.A. 87, 6833-6837, 1990

A;Title: Molecular cloning of cDNA for the human tumor-associated antigen CO-029 and A;Reference number: A36056; MUID:90370878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;12-33/Domain: transmembrane #status predicted <TM1>
F;34-52/Domain: extracellular #status predicted <EX1>
F;53-78/Domain: transmembrane #status predicted <TM2>
F;79-62/Domain: intracellular #status predicted <CY2>
F;83-107/Domain: transmembrane #status predicted <TM3>
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F;2-11/Domain: intracellular #status predicted <CYI>
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A; Residues: 1-237 <SZA>
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C;Date: 16-Nov-1990 #sequence_revision 09-Aug-1996 #text_change 05-Sep-1997
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tumor-associated antigen CO-029 - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                     141 ATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTTTCTGTGTGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 AGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATGGGGCATCCTTTC
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                                                           eLeuIleLeuAlaLeuAlaIleTrpValArgValSerAsnAspSer...G
TGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTG
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                                                                                                                                                                                                   IleLysTyrSerMetPheThrPheAsnPheLeuPheTrpLeuCysGlyIl 24
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Ratio:
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1.790
65.126
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A;Molecule type: mRNA
A;Residues: 1-281 <CLA>
A;Residues: 1-281 <CLA>
A;Cross-references: EMBL:X14046; NID:g29793; PID:g29794
A;Cross-references: EMBL:X14046; NID:g29793; PID:g29794
A;Cross-references: EMBL:X14046; NID:g29793; PID:g29794
A;Classon, B.J.; Williams, A.F.; Willis, A.C.; Seed, B.; Stamenkovic, I.
J. Exp. Med. 169, 1497-1502, 1989
A;Title: The primary structure of the human leukocyte antigen CD37, a species homologue A;Reference number: JL0093; MUID:89176904
A;Accession: JL0093
                                                                                                                                                                                                                                                                                               C;Date: 03-Feb-1994 #sequence_revision 09-Aug-1996 #text_change 05-Sep-1997 C;Accession: A47629; JL0093; JC1500 R;CLasson, B.J.; Williams, A.F.; Willis, A.C.; Seed, B.; Stamenkovic, I. J. Exp. Med. 172, 1007, 1990 A;Reference number: A47629 A;Contents erratum A;Accession: A47629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell surface glycoprotein CD37 - human N;Alternate names: leukocyte antigen CD37 C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pirl:A47629
Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 lnGluAlaIleIleValPheGlnGluGluPheLysCysCysGlyLeuVal 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGCTGTGGCTTCACC 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTTGGTGTACACCACAATGGCTGAGCACTTCCTG.....ACGTTGCT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTCATCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uGlyCysCysGlyAlaIleLysGluSerArgCysMetLeuLeuLeuPheP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTTGGTTTCCT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lnAlaIlePheGlySerGluAspValGlySerSerSerTyrValAlaVal 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asp...IleLeuIleAlaValGlyAlaIleIleMetIleLeuGlyPheLe 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213
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C;Superfamily: CD9 antigen
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lymphocyte; transmembrane protein
F;1-12/Domain: intracellular #status predicted <CY1>
F;13-38/Domain: transmembrane #status predicted <EX1>
F;39-59/Domain: extracellular #status predicted <EX1>
F;60-80/Domain: intracellular #status predicted <TM3>
F;60-80/Domain: intracellular #status predicted <TM3>
F;86-110/Domain: transmembrane #status predicted <TM3>
F;86-110/Domain: extracellular #status predicted <TM3>
F;111-241/Domain: extracellular #status predicted <TM4>
F;242-267/Domain: extracellular #status predicted <TM4>
F;242-267/Domain: intracellular #status predicted <TM4>
F;242-267/Domain: intracellular #status predicted <TM4>
F;268-278/Domain: intracellular #status predicted <CY3>
F;268-278/Domain: intracellular #status p
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A;Gene: GDB:CD37
A;Cross-references: GDB:138750; OMIM:151523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-228,'AARRASRSGCTTT', 242,'FP' <CL2>
A;Experimental source: patient with chronic lymphocytic leukemia
C;Comment: This antigen is expressed abundantly on B lymphocytes and is also seen at
C;Comment: This antigen inhibits the activation of B-cells induced by CD20 antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-030-606-111 x A47629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;170,183,188/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: A47629
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                                                                                                                                                                                                                                                                                                                                         113
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                                                                                                                                                                                                                                                                                                                                                                                                                        408 ATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 TTTGCTCATCTTTCTGTGTGGTGCAGCCCTGTTGGCAGTGGGCATCTGGG
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ValGlnPheGlnLeuArgCysCysGlyTrpHisTyrProGlnAspTrpPh 162
                                                                               ACCATGAAAGGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGA 598
                                                                                                                                                                                                                                                 ATTATGGTTCCCAGGAAGACTTCACT.....CAAGTGTGGAACACC
                                                                                                                                                                                                                                                                                                                                    aGlnLeuGluArgSerLeuArgAspValValGluLysThrIleGlnLys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuPheAlaThrGlnIleThrLeuGlyIleLeuIleSerThrGlnArgAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euLysGluLeuArgCysLeuLeuGlyLeuTyrPheGlyMetLeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leLeuIleAspLysThrSerPheValSerPheValGly......
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                                                                                                                                                                  ..TyrGlyThrAsnProGluGluThrAlaAlaGluGluSerTrpAspTyr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....LeuAlaPheValProLeuGlnIleTrpSerLysValLeuAlaIl 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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Gaps: 7
Percent Identity: 26.573
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GGACTCACCCTACTTCAAAGAGAACAGTGCC....

.TTTCCCC

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F:11-36/Domain: transmembrane #status predicted <TM1>
F:37-54/Domain: extracellular #status predicted <EX1>
F:55-55/Domain: transmembrane #status predicted <CM2>
F:76-80/Domain: intracellular #status predicted <CY2>
F:81-106/Domain: transmembrane #status predicted <TM3>
F:107-181/Domain: extracellular #status predicted <EX2>
F:182-204/Domain: transmembrane #status predicted <TM4>
F:205-219/Domain: intracellular #status predicted <TM4>
F:205-219/Domain: intracellular #status predicted <CY3>
                                                                                                                                                                                                                                                                                                      A;Gene: GDB:CD53; MOX44
A;Cross references: GDB:127521; OMIM:151525
A;Map position: 1p21-1p13.3
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: intracellular #status predicted <CX1>
E;1-10/Domain: intracellular #status predicted <CX1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M60871; NID:g180140; PID:g180141
R;Angelisova, P.; Vlcek, C.; Stefanova, I.; Lipoldova, M.; Horejsi, V.
Immunogenetics, 281-285, 1990
A;Title: The human leucocyte surface antigen CD53 is a protein structurally similar
A;Reference number: A45872; MUID:91055810
A;Accession: A45872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immunol. 145, 4322-4325, 1990
A:Title: Identification and analysis of cDNA clones encoding CD53. A pan-leukocyte antiga; Reference number: A37243; MUID:91079522
A:Accession: A37243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hemopoletic cell surface glycoprotein CD53 - human N;Alternate names: pan·leukocyte surface antigen CD53 C;Species: Homo sapiens (man) C;Date: 30-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 18-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-219 < ANG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-219 < AMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M37033; NID:g180142; PID:g180143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A37243; A45872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir1:A37243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
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   ,148/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sSerAlaAspIleCysAlaValProAlaGluSerHisIleTyrArg...G 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laArgTyr 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGTTGCTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGTCACC 764
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seq_name: pir1:I38016
seq_documentation_block:

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alignment_block:
US-09-030-606-111 x A37243
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
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                                                TGTATCTGTACTGCAATCTA 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           snSerThrLysAlaAlaTrpAspSerIleGlnSerPheLeuGlnCysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rValAlaLysGlyLeuThrAspSerIleHisArg...TyrHisSerAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt eMetValValAlaPheLeuGlyCysMetGlySerIleLysGluAsnLysC}
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                                                                                          eIleThrIleCysValCysValIleGluValLeuGlyMetSerPheAlaL
                                                                                                                                      TGTGGCAGCTGGAATTGGGGGGCCTCGAGCTGGCTGCCATGATTGTGTCCA 822
                                                                                                                                                                                TyrAlaLysAlaArgLeuTrpPheHisSerAsnPheLeuTyrIleGlyIl 187
                                                                                                                                                                                                                               .....ProSerAspArgLysValGluGlyCys
                                                                                                                                                                                                                                                                                                                       ATGAAACCTGCACCAAGCAAAAGGCTCACGACCAAAAAGTAGAGGGTTGC
                                                                                                                                                                                                                                                                                                                                                                 .ThrSerGlyProProAlaSerCys...
                                                                                                                                                                                                                                                                                                                                                                                                           CAGTGCCTTTCCCCCATTCTGTTGCAATGACAACGTCACCAACACAGCCA 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyIleAsnGlyThrSerAspTrp..... 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAAAGAGAA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGCAGCTGCTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysLeuLeuMetSerPhePheIleLeuLeuLeuIleIleLeuLeuAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ........LeuThrLeuGlyAsnValPheValIleValGlySerIleIl
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A:Cross-references: EMBL:X62654; NID:g430755; PID:g430756
R:Hotta, H.; Ross, A.H.; Huebner, K.; Isobe, M.; Wendeborn, S.; Chao, M.V.; Ricciardi, l Cancer Res. 48, 2955-2962, 1988
A:Title: Molecular cloning and characterization of an antigen associated with early stag A:Reference number: S01418; MUID:88210273
A:Accession: S01418
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-238 <WAN>
A; Cross-references: GB:S93788; NID:g246538; PID:g246539
A; Experimental source: uveal melanoma
A; Note: sequence extracted from NCBI backbone (NCBTW-CC: Genetics:
A;Gene: GDB:CD63; MLA1
A;Cross-references: GDB:120186; OMIM:155740
A;Cross-references: GDB:120186; OMIM:155740
A;Introns: 27/3; B5/3; 110/3; 142/3; 189/3; 217/3
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
C;Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F;2-238/Product: melanoma-associated antigen ME491 #status experimental <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanoma-associated antigen CD63 - human

N;Alternate names: antigen ME491; lysosomal membrane glycoprotein CD63; ME491/CD63
C:Species: Homo sapiens (man)
C:Date: 17-May-1996 #sequence_revision 09-Aug-1996 #text_change 26-Feb-1999
C:Accession: I38016; S01418; A39514; B35826; A61177; A61173; A56782
R:Hotta, H; Miyamoto, H.; Hara, I.; Takahashi, N.; Homma, M.
Biochem. Biophys. Res. Commun. 185, 436-442, 1992
A;Title: Genomic structure of the ME491/CD63 antigen gene and functional analysis c
A;Reference number: I38016; MUID:92287132
A;Accession: I38016
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: GB:M58485
R:Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, DNA Cell Biol. 9, 479-485, 1990
A:Title: Characterization of three abundant mRNAs from human ovarian granulosa cells. A:Reference number: A35826; MUID:91025550
A:Accession: B35826
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R;Metzelaar, M.J.; Wijngaard, P.L.J.; Peters, P.J.; Sixma, J.J.;
J. Biol. Chem. 266, 3329-3245, 1991
A;Title: CD63 antigen. A number: Reference number: A39514; MUID:91131632
A;Accession: A39514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-238 < RAP;
A; Cross-references: GB: M59907; NID: g189383; PID: g189384
A; Note: the authors did not translate the codons for residues
R; Azorsa, D.O.; Hyman, J.A.; Hildreth, J.E.K.
Blood 78, 280-284, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: An ocular melanoma-associated antigen. Molecular characterization A;Reference number: A56782; MUID:92181348
A;Accession: A56782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 2-8, 'x', 10-16, 'xx', 19-21 <HIL>
R; Wang, M.X.; Earley Jr., J.J.; Shields, J.A.;
Arch. Ophthalmol. 110, 399-404, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Title: Characterization of a novel self-associating A;Reference number: A61173
A;Accession: A61173
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 2-68,'p',70-238 <AZO>
R;Hildreth, J.E.K.; Derr, D.; Azorsa, D.O.
Blood 77, 121-132, 1991
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A; Residues: 2-68, 'P',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: CD63/Pltgp40: a platelet activation antigen identical A;Reference number: A61177; MUID:91300080 A;Accession: A61177
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A; Residues: 1-238 <MET>
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A; Residues: 1-238 <HOT>
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                                                                                                                                                                                                                                                                                                                                        NCBI backbone (NCBIN:93788,
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                                                                                                                                                                                                                                                                                                                                        NCBIP: 93790)
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F;36-51/Domain: extracellular #status predicted <EX1>
F;52-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-202/Domain: extracellular #status predicted <TM3>
F;104-202/Domain: transmembrane #status predicted <TM4>
F;203-228/Domain: transmembrane #status predicted <TM4>
F;229-238/Domain: intracellular #status predicted <TM4>
F;2103-218/Domain: intracellular #status predicted <TM4>
F;2103-218/Domain: intracellular #status predicted <TM4>
F;130,150,172/Binding site: carbohydrate (Asn) (covalent)
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                                                      690 CAAAAGGCTCACGACCAAAAAGTAGAGGGTTGCTTCAATCAGCTTTTGTA
                                                                                                       168 erCysCys...IleAsnValThrValGlyCysGlyIleAsnPheAsnGlu
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                                                                                                                                                                                                           rAspTrpGluLysIleProSerMetSerLysAsnArgVal...ProAspS
                                                                                                                                                                                                                                                               GGATTTTGAGGACTCACCCTACTTCAAAGAGAACAGTGCCTTTCCCCCCAT
                                                                                                                                                                                                                                                                                                                LeuAspArgMetGlnAlaAspPheLysCysGlyAlaAlaAsnTyrTh
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                                                                                                                                                                                                                                                                                                                                                                                                                       .....GluAsnTyrProLysAsnAsnHisThrAlaSerIle
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A;Molecule type: mRNA
A;Residues: 1-219 <BEL>
A;Cross-references: GB:M$7276; NID:g205897; PID:g205898
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <CY1>
F;11-96/Domain: transmembrane #status predicted <CYM1>
F;37-54/Domain: extracellular #status predicted <EXI>
F;37-54/Domain: transmembrane #status predicted <CY2>
F;74-79/Domain: transmembrane #status predicted <CY2>
F;80-106/Domain: transmembrane #status predicted <CY3>
F;80-106/Domain: transmembrane #status predicted <CY3>
F;80-106/Domain: transmembrane #status predicted <CY3>
F;107-118/Domain: transmembrane #status predicted <CY3>
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Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leukocyte antigen Ox-44 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Aug-1991 #sequence_revision 09-Aug-1996 #text_change 05-Sep-1997
C;Accession: A39574
R;Bellacosa, A.; Lazo, P.A.; Bear, S.E.; Tsichlis, P.N.
Mol. Cell. Blol. 11, 2864-2872, 1991
A;Title: The rat leukocyte antigen MRC OX-44 is a member of a new family of cell surface A;Reference number: A39574; MUID:91203909
A;Accession: A39574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
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273
                                                                                                                                                                                                                                                                                                                    223 TCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCC 272
                                                                                                                                                                                                                                                                                                                                                                                  123 ATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 rIleArg 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 laPheValGluValLeuGlyIleValPheAla......
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                                                                                                            47
                                                                                                                                                                                                                                               36 alGlnAsnThr......46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 MetSerSerLeuLysLeuLeuLysTyrValLeuPhePhePheAsnPheLe
                                                                                                         LeuProPheLeuThrLeuGlyAsnValLeuValIleValGlySerIleIl
                                                                                                                                                                          ATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACATCCGAACTAATGCAGTCACCGTGGGTGGTGGCAGCTGGAATTG 789
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1.603
62.140
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Gaps: 6
Percent Identity: 24.691
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                                                                                                         63
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63 373	^	
423		
	vaiThrLeuAlaIleLeuLeuPheValTyrGluLysLy	
473 109	CCTGACGTTGCTGGTAGTGCCTGCCATCAAGAAAGATTATG 513 ::::: ::: :::::::::::::::::::::::	
514 126	GTTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGCTC 563 ::::::: 	
564 143	AAGTGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTT 613 ::: GlnCysCysGlyValAsnGlySerSerAspTrpIleSerGly 156	
614	CAAAGAGAACAGTGCCTTTCCCCCCATTCTGTTGC	
157		
664 166	ACACAGCCAATGAAACCTGCACCAAGCAAAAGGCTCACGACCAAAAAGTA 713	
714	GAGGGTTGCTTCAATCAGCTTTTGTATGACATC	
764		
184	rIleGlyIleValThrIleCysValCysValIleGlnValLeuGlyMetS 201	
814 201	TTGTGTCCATGTATCTGTACTGCAATCTA 842 	
seq_name:	1	
seq_document; 23K integral N;Alternate; C;Species: S C;Date: 28-0	<pre>Imentation_block: inentation_block: inentation_block: inentation_block: inentation_protein - fluke (Schistosoma mansoni) intentation Sm23 inentation_block: inentation_bl</pre>	-1997
R; Wright, M. J. Immunol. A; Title: An A; Reference	M.D.; Henkle, K.J.; Mitchell, G.F. 1. 144, 3195-3200, 1990 1. 144, 3195-3200, 1990 An immunogenic M-r 23,000 integral membrane protein of Schis ce number: A43522; MUID:90217533	tosoma mansoni w
A; Molecule A; Residues: A; Cross-ref A; Note: obs	Molecule type: mRNA Residues: 1-218 <mriy at="" cross-references:="" gb.m34453;="" is="" molecular="" mos<="" nid:g161029;="" note:="" observations="" of="" pid:g161030="" protein="" suggest="" td="" this="" weight=""><td>st lightly glyc</td></mriy>	st lightly glyc
C; Keyworc F; 1-13/D F; 14-36/I F; 14-36/I F; 37-56/I F; 78-82/I F; 78-82/I F; 183-108 F; 183-108 F; 184-20	tein cted <cy <c<="" <cy="" cted="" td=""><td></td></cy>	
F;207-218 F;165/Bir	9.5	

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alignment_block:
US-09-030-606-111 x A43522
seq_name: pir1:A35649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 ATCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTT 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 CAATTTGCTCATCTTTCTGTGTGGTGCAGCCCTGTTGGCAGTGGGCATCT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 GGAGCCACCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 yrValGluValLysPheSerGlnTyrGlyAspAsnLeuHisLysValTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 uAsnIleIleCysLeuLeuCysSerLeuValLeuIleGlyAlaGlyAlaT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GlyThrGlyMetArgCys.....LeuLysSerCysValPheValLe
                                                                                                                                                                                                                                                                                                                                     ysGluGluAsnLeuThrTyrThr.....169
                                                                                                                                                                                                                                                                                                                                                                                          GCAATGACAACGTCACCAACACAGCCAATGAAACCTGCACCAAGCAAAAG 695
                                                                                                                                                                                                                                                                                                                                                                                                                                          rArgGlyAsn......ValProAlaSerCysL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuIleGlnSerSerPheHisCysCysGlyAlaLysGlyProAspAspTy 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTC
                                                                                             TCGAGCTGCCATGATTGTGTCCATGTATCTG 830
                                                                                                                                             uLysArgAsnLeuValIleValAlaCysValAlaPheGlyValCysPheP
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                                                                                                                                                                                                                                             GCTCACGACCAAAAAGTAGAGGGTTGCTTCAATCAGCTTTTGTATGACAT 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAGGACTCACCCTACTTCAAAGAGAACAGTGCCTTTCCCCCCATTCTGTT 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCACCATGAAAGGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laLeuAspLys......ProThrLysGluIleThrGluPheMetAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCAAGAAAGATTATGGTTCCCAGGAAGACTTCACTCAAGTGTGGAAC 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....IleIleValValGlyValIleIleLeuIleValSerPheLeuGlyC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTCCTGGGCT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....GGGCCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTGGGCTA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ysCysGlyAlaIleLysGluAsnValCysMetLeuTyrMetTyrAlaPhe
                                                heGlnLeuLeuSerIleValIleAlaCysCysLeu 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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1.709
56.735
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A;Gene: GDB:TAPA1

A;Gene: GDB:TAPA1

A;Cross references: GDB:135038; OMIM:186845

A;Map position: 11p15.5-11p15.5

C;Superfamily: CD9 antigen

C;Reywords: transmembrane protein

C;Reywords: transmembrane #status predicted <CY1>
F;2-11/Domain: intracellular #status predicted <TM1>
F;36-57/Domain: extracellular #status predicted <EX1>
F;86-84/Domain: transmembrane #status predicted <CY2>
F;85-88/Domain: transmembrane #status predicted <CY2>
F;89-113/Domain: transmembrane #status predicted <CY2>
F;114-203/Domain: extracellular #status predicted <CY3>
F;204-230/Domain: transmembrane #status predicted <CY3>
F;231-236/Domain: intracellular #status predicted <CY3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Oren, R.: Takahashi, S.: Doss, C.: Levy, R.: Levy, S.
Mol. Cell. Biol. 10, 4007-4015, 1990
A;Title: TAPA-1, the target of an antiproliferative antibody, defines a new family of A;Reference number: A35649; MUID:90318365
A;Recession: A35649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell surface protein TAPA-1 - human
N;Alternate names: target of antiproliferative antibody (TAPA) 1
C;Species: Homo sapiens (man)
C;Date: 28-Sep-1990 #sequence_revision 09-Aug-1996 #text_change 18-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-236 <ORE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: A35649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: A35649 from: 1 to: 236
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                                                     122 pValLysGlnPheTyrAspGlnAlaLeuGlnGlnAlaValValAspAsp.
                                                                                                                                                                                                                                                                                                                                             373
                                                                                                                                                                                                                                                                                                                                                                                                                             323 CTTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 CAGTTTGTCAACGTGGGC...TACTTCCTCATCGCAGCCGGCGTTGTGGT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 GGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGT...GCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 TCTGTGTGGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT
                                                                                                                                                                   106 ValAlaAlaGlyIleTrpGlyPheValAsnLysAspGlnIleAlaLysAs
                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 pLeuAlaGlyGlyValIleLeuGlyValAlaLeuTrpLeuArgHisAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 CysThrLysCysIleLysTyrLeuLeuPheValPheAsnPheValPheTr
                                                                                                                                                                                                                   GTTGCAGCTGCTGGTCGCCTTGGTGTACACCACAATG......
ATGGTTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGG
                                                                                                           GTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTGAG 422
                                                                                                                                                                                                                                                                                                                                                                                               tMetPheValGlyPheLeuGlyCysTyrGlyAlaIleGlnGluSerGlnC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnThrPheTyrValGlyIleTyrIleLeuIleAlaValGlyAlaValMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roGlnThrThrAsnLeuLeuTyrLeuGluLeuGlyAspLysProAlaPro
                                                                                                                                                                                                                                                                                 ysLeuLeuGlyThrPhePheThrCysLeuValIleLeuPheAlaCysGlu
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1.616
59.514
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Percent Identity: 29.960
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F;111/Domain: intracellular #status predicted <TM1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-51/Domain: extracellular #status predicted <TM2>
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F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-202/Domain: extracellular #status predicted <TM3>
F;203-228/Domain: transmembrane #status predicted <TM4>
F;209-238/Domain: intracellular #status predicted <TM4>
F;209-238/Domain: intracellular #status predicted <TM4>
F;215-130,150,172/Binding site: carbohydrate (Asn) (covaler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Oct-1994 *sequence_revision 09-Aug-1996 *text_change 26-Feb-1999
C;Accession: JC2297
R;Sohma, Y; Suzuki, T.; Sasano, H.; Nagura, H.; Nose, M.; Yamamoto, T.
Cell Struct. Funct. 19, 219-225, 1994
A;Title: Increased mRNA for CD63 antigen in atherosclerotic lesions of Watanable A;Reference number: JC2297; MUID:95120837
A;Accession: JC2297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Experimental source: aorta
C:Superfamily: CD9 antigen
C:Keywords: 9lycoprotein: lysosome; surface antigen;
F:1-11/Domain: intracellular #status predicted <CYI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
CD63 antiage - ----
                                                                                                                                                                                                                                                                                                alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-238 <SOH>
A;Cross-references: DDBJ:D21264; NID:g684973; PID:d1005337; PID:g684974
                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir1:JC2297
                                                                                                                                                                                                            Align seg 1/1 to:
                                                                                                                                                                                                                                                                     US-09-030-606-111 x JC2297
                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     561
                                 173 CATCTTTCTGTGTGCTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 heGluMetIleLeuSerMetValLeuCysCysGlyIleArg 231
                                                                                                                                                123 ATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCCATGATTGTGTCCATGTATCTGTACTGCAATCTACAA 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aAlaIleValValAlaValIleMet.......IleP 218
                                                                                       MetLysCysValLysPhe.....LeuLeuTyrValLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCAGTCACCGTGGGTGTGTGGCAGCTGGAATTGGGGGCCTCGAGCTGG 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnLysIleAspAspLeuPheSerGlyLysLeuTyrLeuIleGlyIleAl 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAAAGTAGAGGGTTGCTTCAATCAGCTTTTGTATGACATCCGAACTAA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lLeuLysAsnAsn.....LeuCysProSerGlySerAsnI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCAAAGAGAACAGTGCCTTTCCCCCATTCTGCTTGCAATGACAAC.... 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..GTCACCAACACAGCCAATGAAACCTGCACCAAGCAAAAGGCTCACGAC 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuAspCysCysGlySerSerThrLeuThrAlaLeuThrThrSer...Va 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
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1.523
57.196
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   CTGTTGGCAGTGGGCATCTGGG 216
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26.937
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R:Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Blochem. 112, 63-67, 1992
A:Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial A:Reference number: JX0221; MUID:93054422
                                                                                                                              CD9 antigen - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 20-Mar-1998
                                                                                                                  C; Accession: JX0221
                                                                                                                                                                                                                                 seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505 AAGATTATGGTTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 CICATCITCATIGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACAC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 lLysSerIleArg
                                                                                                                                                                                                                                                                                                                                                                                                               884 GGGAACTGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784 GAATTGGGGGCCTCGAGCTGGCTGCCATGATTGTGTCCATGTATCTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584 CTATACGGATTTTGAGGACTCACCCTACTTCAAAGAGAACAGTGCCTTTC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 LeuIleLeuAspArgMetGlnLysAspPheThrCysCysGlyAlaAlaAs 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 AGTGCCATGCAGTTTGTCAACGTGGGCTACTTCCTC......AT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAATCTACAATAAGTCCACTTCTGCCTCTGCCACTACTGCCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  valLysPheAsnValLysAspIleTyrValGluGlyCysValGluLysIl 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCATTCTGTTGCAATGACAACGTCACCAACACAGCCAATGAAAACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ysAspPheArgGlnGlnMetGlnAsnTyrSerThrAspAsnGlnThrAla 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTC 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAAGCAAAAGGCTCACGACCAAAAAGTAGAGGGTTGCTTCAATCAGCT 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roAspSerCysCys.....ValAsnValThrSerGlyCysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nTyrThrAspTrpAlaThrIleProGlyMetThrArgAspArgVal...P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gAspLys...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eAlaValGlyAlaPheLeuPheLeuValAlaPheValGlyCysCysGlyT
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                                                                                                                                                                                                                                                                                                                                                                                                               896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....CysCysLeuVa
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C.Keywords: glycoprotein; transmembrane protein F:2-236/Product: CD9 antigen #status predicted <MAT>F:2-11/Domain: intracellular #status predicted <CY1>F:12-35/Domain: transmembrane #status predicted <TM1>F:36-53/Domain: extracellular #status predicted <EX1>F:36-53/Domain: extracellular #status predicted <CM2>F:57-80/Domain: intracellular #status predicted <CY2>F:81-109/Domain: intracellular #status predicted <CY3>F:81-109/Domain: transmembrane #status predicted <CY3>F:81-109
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A;Molecule type: mRNA
A;Residues: 1-26 <MAR>
A;Cross references: GB:M81720; NID:g162820; PID:g162821
A;Cross references: ocular ciliary epithelial cell
C;Superimental source: ocular ciliary epithelial cell
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
E;2-226/Product: CD9 antigen #status predicted <MAT>
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US-09-030-606-111 x JX0221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: JX0221 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;110-192/Domain: extracellular #status predicted <EX2>;119-219/Domain: transmembrane #status predicted <TM4>;20-226/Domain: intracellular #status predicted <CY3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355
                                                                                                575 CTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAAAGAGAACA 624
                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 CTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACAC 454 ::::|||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 CCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTGGGCTACTTCCTCAT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 TGGGCATCTGGGTGTCAATCGATGGGGCATCCTTTCTGAAGATCTTCGGG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 GATCCTCTTCAATTTGCTCATCTTTCTGTGGTGCAGCCCTGTTGGCAG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 CCCTGAACAGGAGCCACCATGCAGTGCTTCAGTCATTAAGACCATGAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 CGCAGCCGCGTTGTGGTCTTTGCTCTTGGTTTCCTGGGCTGCTATGGTG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 GlnGluAsnAspSerSerPheTyrThrGlyVal...TyrIleLeuIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 laValGlnGluSerGlnCysMetLeuGlyLeuPhePheSerPheLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 uPheGlyPheAsnPheIlePheTrpLeuAlaGlyIleAlaValLeuSerV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ProValLysGlyGlyThr...LysCys......IleLysTyrLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValilePheAlaIleGluValAlaAlaAlaIleTrpGly.....TyrSe 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eGlyAlaGlyAlaLeuMetMetLeuValGlyPheLeuGlyCysCysGlyA
                                                                                                                                                                                                ProGlnArgGluThrLeuLysAlaIleHisIleAlaLeuAspCysCysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGATTATGGTTCCCAGGAAGACTTCACTCAAGTGTGGAAC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alGlyLeuTrpLeuArgPheAspSerGlnThr...LysSerIlePheGlu
yLeuThrGlyValProGlu.....
                                                                                                                                                                                                                                                                                                ysPheTyr.....GluAspThrTyrAsnLysLeuLysAsnLysAspGlu 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
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1.577
57.752
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Gaps: 11
Percent Identity: 28.682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545
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alignment_block:

Percent Similarity:

Quality: Ratio:

235.00 1.546 57.358

Length: 265
Gaps: 10
Percent Identity: 26.792

US-09-030-606-111 x A46508

:

Align seg 1/1 to: A46508 from: 1

123 ATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCT 172

. 6

7 MetLysCysValLysPhe.....LeuLeuTyrValLeuLe 18

217 TGTCAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCC

18 uLeuAlaPheCysAlaCysAlaValGlyLeuIleAlaIleGlyValAlaV

35

173 CATCTTTCTGTGTGCGCAGCC.....CTGTTGGCAGTGGGCATCTGGG 216

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C:Superfamily: CD9 antigen
(;Keywords: glycoprotein; lysosome; mast cell; surface antigen; transmembrane protein
F:1-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-51/Domain: extracellular #status predicted <EX1>
F:36-51/Domain: transmembrane #status predicted <CY2>
F:77-80/Domain: transmembrane #status predicted <CY2>
F:77-80/Domain: transmembrane #status predicted <CY3>
F:81-103/Domain: transmembrane #status predicted <EX3>
F:104-202/Domain: transmembrane #status predicted <TM4>
F:209-238/Domain: intracellular #status predicted <TM4>
F:209-238/Domain: intracellular #status predicted <TM4>
F:209-238/Domain: intracellular #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD63/ME491 antigen homolog - rat
N;Alternate names: mast cell antigen AD1
C;Species: Rattus norregicus (Norway rat)
C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 05-Sep-1997
C;Accession: A46508; S16776
R;Nishikata, H.; Oliver, C.; Mergenhagen, S.E.; Siraganian, R.P.
J. Immunol. 149, 862-870, 1992
A;Title: The rat mast cell antigen AD1 (homologue to human CD63 or melanoma antigen M A;Reference number: A46508; MUID:92340890
A;Accession: A46508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X61654; NID:g55601; PID:g55602
A;Note: this antigen was found localized to mast cells in tissue samples, but was ind A;Note: sequence extracted from NCBI backbone (NCBIN:109346, NCBIP:109349)
C;Comment: This heavily glycosylated protein of 50-60% (27% after deglycosylation) is
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-238 <NIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir1:A46508
                                                                                                                                   F;130,150,172/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 MetIleLeuCysCysAlaIleArg 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   822 ATGTATCTGTACTGCAATCTACAA 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 lavalGlyIleGlyIleAlavalValMetIlePheGlyMetValPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772 GTGTGGCAGCTGGAATTGGGGGCCTCGAGCTGGCTGCCATGATTGTGTCC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 sProGluAlaIleAspGluIlePheArgSerLysPheHisIleIleGlyA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    722 CTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGTCACCGTGGGTG 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 AspThrCysProProLysAsnLeuIleAspSerLeuLysThrArgProCy 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675 GAAACCTGCACCAAGCAAAAGGCTCACGACCAA...AAAGTAGAGGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         625 GTGCCTTTCCCCCATTCTGTTGCAATGACAACGTCACCAACACAGCCAAT 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #status predicted
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R;Andria, M.L.; Hsieh, C.L.; Oren, R.; Francke, U.; Levy, S.
J. Immunol. 147, 1030-1036, 1991
A;Title: Genomic organization and chromosomal localization of the TAPA-1 gene.
A;Reference number: A46472; MUID:91318144
A;Accession: A46472
                                                                                                    A; Molecule type: DNA
A; Residues: 1-236 < AND>
                                                                                                                                                                                                                                                                                                                                   N;Alternate names: target of antiproliferative antibody (TAPA) 1
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 22-Jan-1999
C;Accession: A46472
C;Accession: A46472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
cell surface protein TAPA-1 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: pir1:A46472
;Cross-references: GB:S45012; NID:g1679982; PID:g233253
;Experimental source: B-cell lymphoma line 38C13
;Note: seguence extracted from NCBI backbone (NCBIN:44957, NCBIN:44966, NCBIN:45001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  752 TAATGCAGTCACCGTGGGTGGTGGCAGCTGGAATTGGGGGGCCTCGAGC 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       702 GACCAAAAAGTAGAGGGTTGCTTCAATCAGCTTTTGTATGACATCCGAAC 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 leAsnIleThrValGlyCysGlyAsnAspPheLysGluSerThrIleHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 GCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTAC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 GCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 AGTGCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 aPheLeuPheLeuValAlaPheValGlyCysCysGlyAlaCysLysGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 ThrAlaGlySerLeuLeuProVal.....ValIleIleAlaValGlyAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGGTCTTTGCTTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alGlnval....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....CysCysLeuValLysSerIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTTCTGCCTCTGCCACTACTGCCACATGGGAACTGTGAAG 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alLeuGlyIleIlePheSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCTGCCATGATTGTGTCCATGTATCTGTACTGCAATCTACAATAAGTC 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sAsnValLeuLeuValAlaGlyAlaAlaLeuGlyIleAlaPheValGluV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrGln.......GlyCysValGluThrIleAlaAlaTrpLeuArgLy 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAACGTCACCAACACAGCCAATGAAACCTGCACCAAGCAAAAGGCTCAC 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gIleProGlyMetAlaLysAspArgVal...ProAspSerCysCys...I 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCACCCTACTTCAAAGAGAACAGTGCCTTTCCCCCCATTCTGTTGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnLysGluAsnLysCysCysGlyAlaSerAsnTyrThrAspTrpGluAr 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAAAGGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGAGGA 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAAGATTATGGTTCCCCAGGAAGACTTCACTCAAGTGTGGAACACCACC
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F;204-230/Domain: intracellular *status predicted <TM4>
F;231-236/Domain: intracellular *status predicted <TM4>
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                                                                                       186 uGlnGln.Asp......Cys......Cys.....
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                                                                                                                                                                                                                                     170 LeuArgAsnThrLeuCysProSerGlyGlyAsnIleLeuThrProLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                        561 CTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTA 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 TCTGTGTGCTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 GGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGT...GCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AsnThrPheTyrValGlyIleTyrIleLeuIleAlaValGlyAlaValMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 pLeuAlaGlyGlyValIleLeuGlyValAlaLeuTrpLeuArgHisAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 ysLeuLeuGlyThrPhePheThrCysLeuValIleLeuPheAlaCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 tMetPheValGlyPheLeuGlyCysTyrGlyAlaIleGlnGluSerGlnC
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                                                                                                                                                                   GTTGCAATGACAACGTCACCAACACAGCCAATGAAACCTGCACCAAGCAA 692
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845	217IlepheGluMetIleLeuSerMetValLeuCysCysGlyIle 230	204 ulleglyllealaalailevalvalalavalllemet	743 CATCCGAACTAATGCAGTCACCGTGGGTGGTGGTGGCAGCTGGAATTGGGG 792	191HisGlnLysIleAspGluLeuPheSerGlyLysLeuTyrLe 204
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US-09-030-606-111 x CD37_MOUSE
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SwissProt_37:KIR4_HUMAN
SwissProt_37:RDS2_XENLA
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EMBL; U18370; G755242; JOINED.
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C01470;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
LEUKOCYTE ANTIGEN CD37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                   MGD; MGI:88330; CD37.
PROSITE; PS00421; TM4; 1.
PFAM; PF00335; transmembr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOMLINSON M.G., WRIGHT M.D.;
"Characterisation of mouse CD37: cDNA and genomic cloning.";
MOL. IMMUNOL. 33:867-872(1996).
-i- SUBCELUCLAR LOCATION: TYPE III MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTIGENS (TM4 SUPERFAMILY)
                                                                                                                                                                                                                                                                               ANTIGEN;
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CYTOPLASMIC (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                    luGlyCysAlaGlnSerLeuGlnLysTrpLeuHisAsnAsnIleIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGTTGCTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ysSerCysTyrAsnSerThrAlaThrAsnAspSerThrValPheAspLys 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACTCACCCTACTTCAAAGAGAACAGTGCCTTTCCCCCCATTC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTATGGTTCCCAGGAAGACTTCACT.....CAAGTGTGGAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 euLysGluLeuArgCysLeuLeuGlyLeuTyrPheGlyMetLeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCGGCGTTGTGGTTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTA
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                                                                                                                                                                                       rLeuSerIlePheLeuCysArgAsnLeuAspHisValTyrAspArgLeuA
                                                                                                                                                                                                                                                                                   IleValGlyIleCysLeuGlyValGlyLeuLeuGluLeuGlyPheMetTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nLysAlaGlnMetLeuLysAlaAsnGluSerGluGluProPheValProC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaGlnPheGlnLeuArgCysCysGlyTrpGlnSerProArgAspTrpAs 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCATGAAAGGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGA 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erTyrArgThrAsnProAspGluThrAlaAlaGluGluSerTrpAspTyr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuPheAlaThrGlnIleThrLeuGlyIleLeuIleSerThrGlnArgVa 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTTCATTGCTGAGGTTGCAGCTGCTGGTCGCCTTGGTGTACACCAC
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                                                                                         laArgTyr 280
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alignment_block:
US-09-030-606-111 x NAG2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                               Align seg 1/1 to: NAG2_HUMAN
                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACHIBANA 1. BODOROVA J., BERDITCHEVSKI F., ZUTTER M.M., HEMLER M.E.;
"NAG-2, a novel transmembrane-4 superfamily (TM4SF) protein that
complexes with integrins and other TM4SF proteins.";
J. BIOL. CHEM. 273:29181-29189(1997).
-!- SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN.
-!- SUBUNIT: FORMS A COMPLEX WITH INTEGRINS.
-!- TISSUE SPECIFICITY: EXPRESSED IN MULTIPLE TISSUES BUT IS ABSENT IN
BRAIN, LYMPHOID CELLS, AND PLATELETS.
-!- SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                           179 TCTGTGTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG
                                                                                                                                                   129 TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAG2_HUMAN STANDARD; PRT; 238 AA. 014817; 15-JUL-1998 (REL. 36, CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 37, LAST ANNOTATION UPDATE) NOVEL ANTIGEN 2 (NAG-2).

TM4SF7 OR NAG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF022813; G2586350; -. MIM; 602644; -.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                            229 GGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAG
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRANSMEM
                                                           21 pLeuGlyGlyCysGlyValLeuGlyValGlyIleTrpLeuAlaAlaThrG
                                                                                                                     5 CysLeuGlnAlaValLysTyrLeuMetPheAlaPheAsnLeuLeuPheTr
lnGlySerPheAlaThrLeu.
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                                                                                                                                                                                                                                                                                      Quality:
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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6
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 SerSerSerPhePro
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seq_name: SwissProt_37:CD37_RAT
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CD37_RAT STANDARD;
                                                    MEDLINE: 90354767.

CLASSON B.J., WILLIAMS A.F., WILLIS A.C., SEED B., STR

"The primary structure of the human leukocyte antigen
homologue of the rat MRC OX-44 antigen.";

J. EXP. MED. 172:1007-1007(1990).
                                                                                                                                                                                                                                                                         01-JUL-1993 (REL. 26, C
01-JUL-1993 (REL. 26, L
01-FEB-1995 (REL. 31, L
LEUKOCYTE ANTIGEN CD37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
-1- SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN
-1- TISSUE SPECIFICITY: B LYMPHOCYTES.
-1- SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE
                                                                                                                                                                                                                    EUKARYOTA;
                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
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                                                                                                                                                STRAIN-PVG X DA;
                                                                                                                                                                                                   RODENTIA; SCIUROGNATHI;
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                                                                                                                                                               SEQUENCE FROM N.A.
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26, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                   CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CHI; MURIDAE; MURINAE; RATTUS.
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   TYPE-II MEMBRANE
                                                                                                           STAMENKOVIC I.;
                                                                                          CD37, a species
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alignment_block:
US-09-030-606-111 x CD37_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: CD37_RAT from: 1
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Percent Similarity:
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X53517; G55912; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                            308
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                                                                                                                                                                                                                                                                                                                                                            167 TTTGCTCATCTTTCTGTGTGGTGCAGCCCTGTTGGCAGTGGGCATCTGGG
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                                                                                                                                     358
                                                                                                                                                                                                                                                                                                     217 TGTCAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCC
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                                                                                                                                                                                           AGCCGGCGTTGTGGTCTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTA
                                                                                                                                                                                                                                                AGTGCCATGCAGTTTGTCAACGTG......GGCTACTTCCTCATCGC
                                                                                                                                                                                                                                                                                                                                nLeuPhePhePheValLeuGlyGlyLeuIlePheCysPheGlyThrTrpI
                                                                                                                                                                                                                                                                                                                                                                                       AlaGlnGluSerCysLeuSerLeuIleLysTyrPheLeuPheValPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTIGENS (TM4 SUPERFAMILY).
largLeuGluArgArgValGlnGluLeuValLeuArgThrIle..
                         LeuPheAlaThrGlnIleThrLeuGlyIleLeuIleSerThrGlnArgVa
                                                                               ATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCAC
                                                                                                          euLysGluLeuArgCysLeuLeuGlyLeuTyrPheGlyMetLeuLeuLeu
                                                                                                                                     AGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTC
                                                                                                                                                                 lSerGlyValLeuThrMetAlaLeuAlaLeuLeuGlyCysValGlyAlaL
                                                                                                                                                                                                                                                                           leLeuIleAspLysThrSerPheValSerPheValGly......
                                                                                                                                                                                                                    ....LeuSerPheValProLeuGlnThrTrpSerLysValLeuSerVa
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CYTOPLASMIC (PROBABLE).
SIGNAL-ANCHOR (TYPE-II
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CYTOPLASMIC (PROBABLE).
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seq_name: SwissProt_37:CD82_HUMAN
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01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CD82 ANTIGEN (INDUCIBLE MEMBRANE PROTEIN R2) (C33 ANTIGEN) (IA4)
(METASTASIS SUPPRESSOR KANGAI 1) (SUPPRESSOR OF TUMORIGENICITY-6).
HOMO SAPIENS (HUMAN).
EUKARROTA; METASOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                      and
                                      NISHIMURA M., HINUMA Y., YOSHIE O.;
"C33 antigen recognized by monoclonal antibodies inhibitory to human
"C41 leukemia virus type 1-induced syncytium formation is a member
T cell leukemia virus type 1-induced syncytium formation is a member
of a new family of transmembrane proteins including CD9, CD37, CD53,
                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 93017900.
IMAI T., FUKUDOME K.,
                                                                                                                                                                                                                   "A new superfamily of lymphoid and melanoma cell proteins with extensive homology to Schistosoma mansoni antigen Sm23."; EUR. J. IMMUNCL. 21:377-383(1991).
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                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
IMMUNOL. 149:2879-2886(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                         TAKAGI S., NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                           NAGIRA M.,
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                                                                                                                           FURUSE M.,
                                                                                                                              FUKUHARA
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alignment_block:
                                                                                                                                                                 alignment_scores:
    Quality:
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                                                                                                  US-09-030-606-111 x CD82_HUMAN
                                                                                                                                         Ratio:
Percent Similarity:
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EMBL; X48196; G258295; -.
EMBL; U20770; G806806; -.
EMBL; U67274; G1832296; JOINED.
EMBL; U67268; G1832296; JOINED.
EMBL; U67270; G1832296; JOINED.
EMBL; U67271; G1832296; JOINED.
EMBL; U67271; G1832296; JOINED.
EMBL; U67272; G1832296; JOINED.
EMBL; U67273; G1832296; JOINED.
EMBL; U67273; G1832296; JOINED.
                                                                                                                                                                                                                                CARBOHYD
CONFLICT
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CARBOHYD
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DOMAIN
TRANSMEM
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MEDLINE; 95
DONG J.T.,
                                                  129
                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DONG J;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: ASSOCIATES WITH CD4 OR CD8 AND DELIVERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "KAI1, a metastasis suppressor gene chromosome 11p11.2."; SCIENCE 268:884-886(1995).
179 TCTGTGTGCGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG 228
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                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTIGENS (TM4 SUPERFAMILY).

DATABASS: NAME-PROW; NOTE-CD guide CD82 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd82.htm".
                      CysIleLysValThrLysTyrPheLeuPheLeuPheAsnLeuIlePhePh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNALS FOR THE TCR/CD3 PATHWAY.
SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN
                                                 TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                       S16156;
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95273964.
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Gaps: 11
Percent Identity: 29.851
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II -> MV (IN REF.
DF690722 CRC32;
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                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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seq_documentation_block:
ID CD82_MOUSE STANDA
AC P40237;
DT 01-FEB-1995 (REL. 31.
DT 01-FEB-1995 (REL. 31.
DT 15-JUL-1998 (REL. 36.
DE CD82 ANTIGEN (INDUCII
GN CD82.
OS MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                              seq_name: SwissProt_37:CD82_MOUSE
                     CD82_MOUSE STANDARD; PRT; 266 AA. P40237; O1-FEB-1995 (REL. 31, CREATED) O1-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) CD82 ANTIGEN (INDUCIBLE MEMBRANE PROTEIN R2) CD82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 rgGluAspSerLeuGlnAspAlaTrpAspTyrValGlnAlaGlnValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 nGluMetGlyGlyIleValThrGluLeuIleArgAspTyrAsnSerSerA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426
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MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
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                                                                                                                                                                                                                                                                                                                                                                                                                             euGlyValGlyValGlyValAlaIleIleGluLeuGlyMetValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGCTGCTGTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCT
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                                                                                                                                                                                                                                                          gHis 255
                                                                                                                                                                                                                                                                                                    CTAC 872
                                                                                                                                                                                                                                                                                                                                              SerIle...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGTGTGGCAGCTGGAATTGGGGGCCTCGAGCTGGCTGCCATGATTGTG
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                                                                                                                                                                                                                                                                                                                                                                                   TCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGl 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....AAAGAGAACAGTGCCTTTCCCCCATTCTGT......TGCA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysCysGlyTrpValSerPheTyrAsnTrpThrAspAsnAlaGluLeuMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACGTTG...CTGGTAGTGCCTGCCATCAAGAAAGATTAT...GGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTGAGGTT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tLeuMetGlyPheLeuGlyCysIleGlyAlaValAsnGluValArgCysL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yCysMetGluLysValGlnAlaTrpLeuGlnGluAsnLeuGlyIleIleL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .LeuArgMetGlyAlaTyrValPheIleGlyValGlyAlaValThrMe
                                                                                                                                                                                                                                                                                                                                            CysLeuCysAr
                                           (C33 ANTIGEN) (IA4).
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alignment_block:
US-09-030-606-111 x CD82_MOUSE
                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                  Align seg 1/1 to: CD82_MOUSE
                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94313678.

NAGIRA M., IMAI T., ISHIKAWA I., UWABE K.I., YOSHIE O.;

"Mouse homologue of C33 antigen (CD82), a member of the transmembrane 4 superfamily: complementary DNA, genomic structure, and expression.";
                                                                                                                                                                                                                                                                                                                      CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNALS FOR THE TCR/CD3 PATHWAY.
-!- SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE SPLEEN AND THE
KIDNEY. LOW EXPRESSION IN SKELETAL MUSCLE AND IN THE HEART.
-!- SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE
ANTIGENS (TM4 SUPERFAMILY).
                                                                                 179
                                                                                                                                      129 TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EURARYOTA; METAZOA; CHORDATA; VERTEBBATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
[1]
                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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PROSITE; PS00421; TM4; 1.
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                                                      21
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                                                                                                          CysValLysValThrLysTyrPheLeuPheLeuPheAsnLeuLeuPhePh
ysAsnSerPheIleSerValLeuGlnThrSerSerSerSer
                        GGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAG
                                                     eIleLeuGlyAlaValIleLeuGlyPheGlyValTrpIleLeuAlaAspL
                                                                                TCTGTGTGGGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG
                                                                                                                                                                                                                                                  Quality:
Ratio:
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35
54
73
73
111
228
250
127
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                                                                                                                                                                                                                                  284.00
1.753
58.273
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34
72
72
110
227
227
127
127
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                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                from:
                                                                                                                                                                                                                                     Percent Identity: 28.058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL-ANCHOR; ANTIGEN. CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                      POTENTIAL.
AFF2BE8A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (PROBABLE).
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Gaps:
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6
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51
                         278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN)
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TTTGTCAACGTGGGC...TACTTCCTCATCGCAGCCGGCGTTGTGGTCTT

LeuGlnValGlyAlaTyrValPheIleGlyValGlyAlaIleThrIl

67

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seq_name: SwissProt_37:A15_HUMAN
                                                                                                                                                                                                                                                                            _documentation_block:
                                                                                                                                                                                                                                            A15_HUMAN
P41732;
 MEDLINE;
                                                                                  SURFACE MARKER 1).
SURFACE MARKER 1).
TM4SF2 OR MXS1 OR A15.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                       01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANOTATION UPDATE)
CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA
ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME,
                                                                                                                                                                                                                                                                                                                                              250
                                                                                                                                                                                                                                                                                                                                                                                                                                          789
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                TISSUE-PERIPHERAL BLOOD LYMPHOCYTES; MEDLINE; 93131291.
                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euLeuGlyLeuTyrPheValPheLeuLeuLeuIleLeuIleAlaGlnVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTCGTGACGTTCTTCATCCTCCTCCTCATCTTCATTGCTGAGGTT
                                                                                                                                                                                                                                                                                                                                                                            TCTACAATAAGTCCACTTCTGCCTCTGCCACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGGCCTCGAGCTGCCATGATTGTGTCCATGTATCTGTACTGCAA 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laTrpLeuGlnGluAsnPheGlyIleLeuLeuGlyValCysAlaGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGACATCCGAACTAATGCAGTCACCGTGGGTGGTGGCAGCTGGAATT 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTCACGACCAAAAAGTA.....GAGGGTTGCTTCAATCAGCTTTTGT
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                                                                                CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                               STANDARD;
 SETO M.,
                                                                                                                                                                                                                                                                                                                                          .CysLeuCysArgTyr
 UEDA R.,
                                                                                                                                                                                                                                                             PRT;
                                                                                OMOH
                                                                                                                                                                                                                                                             244
 SAITO
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A
Η.,
 TAKAHASHI
                                                                                               EUTHERIA
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alignment_scores:
    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-030-606-111 x A15_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAKAGI S., FUJIKAWA K., IMAI T., FUKUHARA N., FUKUDOME K., MINEGISHI M., TSUCHIYA S., KONNO T., HINUMA Y., YOSHIE O.; "Identification of a highly specific surface marker of T-cell acute lymphoblastic leukemia and neuroblastoma as a new member of the transmembrane 4 superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN.
-:- TISSUE SPECIFICITY: NOT SOLELY EXPRESSED IN T CELLS. EXPRESSED ACUTE MYELOCYTIC LEUKEMIA CELLS OF SOME PATIENTS.
-:- SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE ANTICENS (TM4 SUPERFAMILY).
                                                                                                            220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 300096;
PROSITE; PSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation of a novel cDNA clone showing ME491/CD63 superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                             19 eValPheTrpIleThrGlyValIleLeuLeuAlaValGlyValTrpGlyL
                                                                                                                                                                                                                                                                   3 ThrLysProValIleThrCysLeuLysThrLeuLeuIleIleTyrSerPh
                                                   ysLeuThrLeuGlyThrTyrIleSerLeuIleAlaGluAsnSerThr...
                                                                                                                                                                                                                   GCTCATCTTTCTGTGTGGTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGT
                                                                                                                                                                                                                                                                                                                               ACCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I
GCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGT
                                                                                                      CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00421; TM4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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64.490
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CYTOPLASMIC (PROBABLE).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

EXTRACELLULAR (PROBABLE).
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seq_name: SwissProt_37:CO02_HUMAN
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                     LINNENBACH A.J.;

"Molecular cloning of cDNA for the human tumor-associated antigen co-029 and identification of related transmembrane antigens.";

PROC. NATL. ACAD. SCI. U.S.A. 87:8833-6837(1990).

-!- SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: GASTRIC, COLON, RECTAL, AND PANCREATIC
                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDAT
TUMOR-ASSOCIATED ANTIGEN CO-029.
                                                                                                                                                                                                                                                                                                                                                                                             CO02_HUMAN
P19075;
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                                                                                                                                            SZALA S., KASAI Y., STEPLEWSKI Z., RODECK U., KOPROWSKI H.,
                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-COLORECTAL CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
                                                                                                                                                                 MEDLINE; 90370878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysGlyValGlnAsnTyrThrAsnTrpSerThrSerProTyrPheLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             snAspGluArgSerArgAlaValAspHisValGlnArgSerLeuSerCys 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluLeuValAlaGlyIleSerGlyPheValPheArgHisGluIleLysAs 113
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 BELONGS TO THE
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FAMILY OF
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TYPE-II MEMBRANE
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alignment_scores:
Quality:
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00421; TM4; 1.
PFAM; PF00335; transmembr
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                  CTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGCTGTGGCTTCACC
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                                                                                                                         GlyAlaValPheLysSerLysSerAspArgIleValAsnGluThrLeuTy
                                                                                                                                                                                                                                 TCTTCATCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTC
                                                                                                                                                                                                                                                                  eLeuIleLeuAlaLeuAlaIleTrpValArgValSerAsnAspSer...G
                                                                                    GGTAGTGCCTGCCATCAAGAAAGATTATGGT...TCCCAGGAAGACTTCA
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                                                                                                                                                                                             heIleGlyLeuLeuIleLeuLeuGlnValAlaThrGlyIleLeu
                                                  rGluAsnThrLysLeuLeuSerAlaThrGlyGluSerGluLysGlnPheG
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1.790
65.126
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Gaps: 7
Percent Identity: 30.252
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CYTOPLASMIC (PROBABLE).
POTENTIAL.
EXTRACELLULAR (PROBABLE).
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CYTOPLASMIC (PROBABLE).
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SIGNAL-ANCHOR (TYPE-II MEMBRANE
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SEQ_documentation_block:
ID A15_MOUSE STANDARD;
AC 062283;
DT 01-NOV-1997 (REL. 35, CREADT 01-NOV-1997 (REL. 35, LAST 01-NOV-1997 (REL. 35, LAST 01-NOV-1997 (REL. 35, LAST 01-NOV-1997 (REL. 37, LAST 01-NOV-1997) (REL. SUMSCHILDS (REL. 1995) (REL. 1995)
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CELL SURFACE GLYCOPROTEIN A15 (PE31) (TALLA HOMOLOG).
TM4ST2 OR MXS1.
TM4ST2 OR MXS1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAGIRA M., ISHIKAWA I., FUJIKAWA K., TAKAGI S., YOSHIE O.; SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DARA BANKS.
-I- SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN.
-I- SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE ANTIGENS (TM4 SUPERFAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D26483; G685221; -. PROSITE; PS00421; TM4; 1. PFAM; PF00335; transmembrane4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 PheIleLysAspPheLeuAlaLysAsnLeuIleIleValIleGlyIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euTyrCysGlnIle 234
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       POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR, CYTOPLASMIC (PROBABLE).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
EXTRACELLULAR (PROBABLE).
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CYTOPLASMIC (PROBABLE).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                         146 CysGlyValGlnAsnTyrThrAsnTrpSerSerSerProTyrPheLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                 570 TGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAAAGA
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                                        tGluThrAsnMetGlyIleIleAlaGlyValAlaPheGlyIleAlaPheS
                                                                                   CCGAACTAATGCAGTCACCGTGGGTGGTGTGGCAGCTGGAATTGGGGGCCC
                                                                                                                           AlaThrLysValAsnGlnLysGlyCysTyrAspLeuValThrSerPheMe
                                                                                                                                                                                                                etAsnGluThrAspCysAsnProLeuAspLeuHisAsnLeuThrValAla
                                                                                                                                                                                                                                                                                                      AGGAAGACTTCACTCAAGTGTGGGAACACCACCATGAAAGGGCTCAAGTGC
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erGlnLeuIleGlyMetLeuLeuAlaCysCysLeu

seq_name:

SwissProt_37:CD37_HUMAN

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alignment_block:
US-09-030-606-111 x CD37_HUMAN
                                                                                           alignment_scores:
                                                         Ratio:
Percent Similarity:
  Align seg 1/1
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CD37_HUMAN STANDARD;
                                                                                                                                           CARBOHYD
                                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                            EMBL; X14046; G29794; -. PIR; JC1500; JC1500. PIR; A47629; A47629.
                                                                                                                                                                                                                                                                                                                                                                        the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSON B.J., WILLIAMS A.F., WILLIS A.C., SEED B., STAMENKOVIC I.; "The primary structure of the human leukocyte antigen CD37, a species homologue of the rat MRC OX-44 antigen."; J. EXP. MED. 169:1497-1502(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD37.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1989 (REL. 11, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LEUKOCYTE ANTIGEN CD37.
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                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                           PROSITE; PS00421; TM4; 1.
PFAM; PF00335; transmembrane4; 1.
                                                                                                                                                                                                                                              MAIN
                                                                                                                                                                                                                                                                       NIAMOC
                                                                                                                                                                                                                                                            RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTIGENS (TM4 SUPERFAMILY).

DATABASE: NAME-PROW; NOTE-CD guide CD37 entry;
www-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd37.htm".
                                                                                Quality:
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 to: CD37_HUMAN
                                                                                                                                                    N; ANTIGEN;
1 12
13 36
37 59
60 74
75 81
112 241
112 241
242 266
267 217
170 170
                                                         271.00
1.633
58.042
                                                                                                                              31703
                                                                                                                                                                                                                                                       TRANSMEMBRANE; SIGNAL-ANCHOR.
CYTOPLASMIC (PROBABLE).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                              MW.
                                                           Percent
  from:
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                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                       CYTOPLASMIC (PROBABLE).
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                                                                                                                                                                           CYTOPLASMIC (PROBABLE)
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Gaps:
Identity:
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   281
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                                                         286
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laArgTyr 280
                                 GCCACTAC 872
                                                                    rLeuSerIlePheLeuCysArgAsnLeuAspHisValTyrAsnArgLeuA
                                                                                          TGTGTCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCT
                                                                                                                                        IleValGlyIleCysLeuGlyValGlyLeuLeuGluLeuGlyPheMetTh
                                                                                                                                                                           luGlyCysAlaGlnGlyLeuGlnLysTrpLeuHisAsnAsnLeuIleSer
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seq_name:

SwissProt_37:CD53_HUMAN

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alignment_block:
US-09:030-606-111 x
                                                                                    alignment_scores
                                        Quality:
Ratio:
Percent Similarity:
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EMBL; M60871; G180141; -
PIR; A37243; A37243.
PIR; A45872; A45872.
MIM; 151525; -
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01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).
CD53 OR MOX44.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 91055810.

ANGELISOVA P., VLCEK C., STEFANOVA I., LIPOLDOVA M., HO
"The human leucocyte surface antigen CD53 is a protein
similar to the CD37 and MRC OX-44 antigens.";
IMMUNOGENETICS 32:281-285(1990).
                                                                                                                                                                                                                                                                                                                          PROSITE; PS00421; TM4; PFAM; PF00335; transmer
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and analysis of CDNA clones encoding CD53. A pan-
leukocyte antigen related to membrane transport proteins.";
J. IMMUNOL. 145:4332-4335(1990).
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                                                                                                                                                                                                                                                                                                             GLYCOPROTEIN;
                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTIGENS (TM4 SUPERFAMILY).

DATABASE: NAME-PROW; NOTE-CD guide CD53 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd53.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN.
TISSUE SPECIFICITY: B CELLS, MONOCYTES, MACROPHAGES, NEUTROPHILS,
SINGLE (CD4 OR CD8) POSITIVE THYMOCYTES, PERIPHERAL T CELLS.
SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                       ; ANTIGEN;
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 CD53_HUMAN
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1.781
62.917
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                                                                                                                                                                                                                                                              TRANSMEMBRANE; SIGNAL-ANCHOR.
CYTOPLASMIC (PROBABLE).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (PROBABLE).
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                                           Percent Identity:
                                                                                                                                                                                                                   CYTOPLASMIC (PROBABLE).
POTENTIAL.
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                                                                                                                                                                                                      EXTRACELLULAR (PROBABLE)
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15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UDDATE)
PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).
                                                                                                                    035566;
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alignment_block:
US-09-030-606-111 x C151_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                Align seg 1/1 to:
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD151.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1096360; CD151.
PROSITE: PS00421; TM4; 1.
PFAM; PF00335; transmembrane4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and expression of mouse homologue of SFA-1/PETA-3 (CD151), a member of the transmembrane 4 superfamily."; BIOCHIM. BIOPHYS. ACTA 1353:125-130(1997).
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HASEGAWA H., WATANABE
                              341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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uAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrI
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                             GGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCT 390
                                                          AlaTyrIleLeuValValAlaGlyValValValMetValThrGlyValLe 77
                                                                         GGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTTCCT 340
                                                                                                                 leSerLeu.....LeuAlaSerSerThr.....TyrLeuAlaThr 60
                                                                                                                                              TGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTG
                                                                                                                                                                                                       AGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATGGGGCATCCTTTC 240
                                                                                                                                                                                                                                     LeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAlaGlyLe
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uGlyCysCysAlaThrPheLysGluArgArgAsnLeuLeuArgLeuTyrP
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                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 28
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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seq_name: SwissProt_37:CD53_MOUSE
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                                                                                                                                                                                                                                      Q61451; Q61721;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE
                                                                                      "Gene structure, chromosomal localization, and prot mouse CD53 (Cd53): evidence that the transmembrane arose by gene duplication."; IMMUNOL. 5:209-216(1993).
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                                                                                                                                                      WRIGHT M.D., ROCHELLE J.M., TOMLINSON M.G., SELDIN M.F WILLIAMS A.F.;
                                                                                                                                                                                                    STRAIN-129
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 GluHisTyr 253
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                                                                                                                                                                                  MEDLINE; 93200067
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                                                                           -!- FUNCTION: MAY BE INVOLVED IN GROWTH REGULATION IN HEMATOPOIETIC
         SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE. ANTIGENS (TM4 SUPERFAMILY).
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SEQUENCE
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CARBOHYD
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DOMAIN
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INIT_MET
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 514 GTTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGCTC
                                                                                                                                                                                                                                                                                                                   273
                                                                                                                                                                                                                                                                                                                                                                              223 TCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCC
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                                                           CCTGACGTTGCTGGTAGTGCCTGCCATCAAG.....AAAGATTATG
                                                                                                                         GTTGCAGCTGCTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTT 472
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                             sLeuAsnThrLeuValAlaGluGlyLeuAsnAspSerIleGlnHisTyrH
                                                                                                                                                        ysLeuLeuMetSerPhePheValLeuLeuLeuIleIleLeuLeuAlaGlu
                                                                                        ValThrIleAlaIleLeuLeuPheValTyr......GluGlnLy
                                                                                                                                                                                                                                                                                  LeuProPheLeuThrLeuGlyAsnIleLeuValIleValGlySerIleIl
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ITE; PS00421; TM4; 1
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BY SIMILARITY.
CYTOPLASMIC (PROBABLE).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
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seq_documentation_block: ID CD63_HUMAN STAN
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01-NOY-1988 (REL. 09, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491) (LYSOSOME-ASSOCIATED CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN MELANOMA-ASSOCIATED CONTRACTOR (CONTRACTOR CONTRACTOR MELANOMA-ASSOCIATED CONTRACTOR (CONTRACTOR CONTRACTOR CONTRACTOR MELANOMA-ASSOCIATED
                                                                                                                                                                          MEDLINE;
RAPP G.,
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
SEQUENCE FROM N.A.
MEDLINE; 92287132.
HOTTA H., MIYAMOTO H., HARA I., TAKAHASHI N., HOMMA M.;
MGTDOMIC Structure of the ME491/CD53 antigen gene and functional
analysis of the 5'-flanking regulatory sequences.";
                                                                                                                                                                                                                                                             "CD63 antigen. A novel lysosomal membrane glycoprotein, cloned
screening procedure for intracellular antigens in eukaryotic of
J. BIOL. CHEM. 266:3239-3245(1991).
                                                                                                                                                                                                                                                                                                                                                                                                            HOTTA H., ROSS A.H., HUEBNER K., ISOBE M., WENDEBORN S., CHAO M.V., RICCIARDI R.P., TSUJIMOTO Y., CROCE C.M., KOPROWSKI H.; "Molecular cloning and characterization of an antigen associated with early stages of melanoma tumor progression.";
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                                                                                                                         granulosa cells
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                                                                                                       NA CELL BIOL. 9:479-485(1990)
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanoma-associated antigen.";
ARCH. BIOCHEM. BIOCHEYS. 242:540-548(1985).
-I- FUNCTION: THIS ANTIGEN IS ASSOCIATED WITH EARLY STAGES OF MELANON
-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. LYSOSOMAL.
-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. LYSOSOMAL.
-I- TISSUE SPECIFICITY: DYSPLASTIC NEVI, RADIAL GROWTH PHASE PRIMARY
MELANOMAS, HEMATOPOIETIC CELLS, TISSUE MACROPHAGES.
-I- SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE; 92181348.
WANG M.X., EARLEY J.J. JR., SHIELDS J.A., DONOSO L.A.;
"An ocular melanoma-associated antigen. Molecular characterization.";
"An ocular melanoma-associated antigen. Molecular characterization.";
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATKINSON B., KOPROWSKI H.; "Isolation and amino terminal sequencing of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 92181348.
                                                                                                                                                                                                                                                                                                                                                       GLYCOPROTEIN;
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DATABASE: NAME-PROW; NOTE-CD guide CD63 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd63.htm"
                                                                                                 Similarity:
          ATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCT
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ANTIGEN; TRANSMEMBRANE; SIGNAL-ANCHOR; LYSOSOME
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (PROBABLE).
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STANDARD;

PRT;

253 ₿

LAST CREATED)

SEQUENCE UPDATE)

seq_name:

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alignment_scores:
Quality:
                                                                                 alignment_block:
US-09-030-606-111 x C151_HUMAN
                                                                                                                                                                                                       Percent Similarity:
                                                         Align seg 1/1
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                                                                                                                                                                                                                  CARBOHYD
CONFLICT
CONFLICT
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DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **HASEGAWA H., UTSUNOMIYA Y., KISHIMOTO K., YANAGISAWA K., FUJITA S.; "SFA-1, a novel cellular gene induced by human T-cell leukemia virus type 1, is a member of the transmembrane 4 superfamily."; J. VIROL. 70:3258-3263(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FITTER S., TETAZ T.J., BERNDT M.C., "MOlecular cloning of cDNA encoding tetra-span antigen, PETA-3.";
BLOOD 86:1348-1355(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U14650; G541613; -. EMBL; D29963; D1006793; -.
                            141 ATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTTTCTGTGGTGC 190
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00335; transmembrane4;
                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00421; TM4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
16 LeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAlaGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTIGENS (TM4 SUPERFAMILY).

DATABASE: NAME-PROW; NOTE-CD guide CD151 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd151.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE
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                                                                                                                                     Ratio:
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58
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63.052
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
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-> S (IN REF. 2).
0E29E7ED CRC32;
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238
                                                                                                   811 TGATTGTGTCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTC 857
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                                                                                                                                                                                                                                                                                                                                                                                                              673 ATGAAACCTGCACCAAGCAAAAGGCTCACGACCAA.....AAAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 leSerLeu.....LeuAlaSerGlyThr....TyrLeuAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 uAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrI
                                                                                                                                                   gValIleGlyAlaValGlyIleGlyIleAlaCysValGlnValPheGlyM
                                                                                                                                                                                                                                                          GluGlyGlyCysIleThrLysLeuGluThrPheIleGlnGluHisLeuAr
                                                                                                                                                                                                                                                                                                          GAG...GGTTGCTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yArgValValProAspSerCysCys......LysThrValV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerGlnAspTrpArgAspSerGluTrpIleArgSerGlnGluAlaGlyGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heIleLeuLeuIleIlePheLeuLeuGluIleIleAlaGlyIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCATCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTC 440
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                                             etIlePheThrCysCysLeuTyrArgSerLeuLysLeuGluHisTyr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....TTTCCCCCATTCTGTTGCAATGACAACGTCACCAACACAGCCA
SwissProt_37:CD53_RAT
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seq_name:

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Seq_documentation_block:
ID CD53_RAT STANDA
AC P24485;
DT 01-MAR-1992 (REL. 21,
DT 01-MAY-1992 (REL. 32,
DT 01-NOV-1997 (REL. 35,
DE LEUKOCYTE SURFACE ANT
DE (LEUKOCYTE ANTIGEN MR
GN CD53 OR OX-44.
OS RATTUS NORVEGICUS (RA
OC EUKARYOTA; METAZOA; C
OC RODENTIA; SCIUROGNATH
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91203909.
                                               CD53 OR OX-44.
RATTUS NORVEGICUS (RAT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
COTTROGNATHI; MURIDAE; MURINAE;
                                                                                                                                   P24485;
01-MAY-1992 (REL. 21, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LEUKCCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN
(LEUKCCYTE ANTIGEN MRC OX-44).
CD53 OR OX-44.
                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                            218
                                                                      MAMMALIA;
RATTUS
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alignment_scores:
Quality:
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CLASSON B.J., WILLIAMS A.F., WILLIS A.C., SEED B., STAMENKOVIC I.:

CLASSON B.J., WILLIAMS A.F., WILLIS A.C., SEED B., STAMENKOVIC I.:

The primary structure of the human leukocyte antigen CD37, a species homologue of the rat MRC OX-44 antigen.";

J. EXP. MED. 169:1497-1502(1989).

-i- FUNCTION: MAY BE INVOLVED IN GROWTH REGULATION IN HEMATOPOIETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BELLACOSA A., LAZO P.A., BEAR S.E., TSICHLIS P.N.;
"The rat leukocyte antigen MRC OX-44 is a member of a new family of cell surface proteins which appear to be involved in growth regulation.";
                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INIT_MET DOMAIN
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PFAM; PF00335; transmembrane4;
GLYCOPROTEIN; ANTIGEN; TRANSME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M57276; G205898; -. PIR; A39574; A39574.
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                                                            223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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TISSUE SPECIFICITY: SPLEEN AND THYMUS, B CELLS, MONOCYTES,
MACROPHAGES, NEUTROPHILS, SINGLE (CD4 OR CD8) POSITIVE THYMOCYTES,
PERIPHERAL T CELLS.
SIMILARITY: BELONGS TO THE FAMILY OF SMALL TYPE-II MEMBRANE
ANTIGENS (TM4 SUPERFAMILY).
                                                                                           uPheTrpValCysGlyCysCysIleLeuGlyPheGlyIleHisLeuLeuV
ATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGT 322
                             alGlnAsnThr...........TyrGlyIleLeuPheArgAsn... 45
                                                            TCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCC 272
                                                                                                                                                       MetSerSerLeuLysLeuLeuLysTyrValLeuPhePheAsnPheLe
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CYTOPLASMIC (PROBABLE).
POTENTIAL.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (PROBABLE).
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8461D7CA CRC32;
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POTENTIAL.
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Database: SPTREMBL_10:*
Database sequences: 201082
Database length: 61543640
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Query: US-09-030-606-111
Query length: 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search time (sec):
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-Q-/cgn2_1/USPT0_spool/US09030606/runat_24091999_171617_29869/app_query.fasta.1
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-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=stat -USER=US09030606
-NCPU=6 -ICPU=3 -WAIT -THREADS=1
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Quality: 1
Ratio:
Percent Similarity: 1
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sp_fung1:094317
sp_mammal:Q29070
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                     GGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAAAGAGAA
                                            luAspPheThrGlnValTrpAsnThrThrMetLysGlyLeuLysCysCys
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seq_documentation_block:

ID 060745 PRELIMINARY; PRT; 241 AA.

O60745;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DT TETRASPAN NET-1.

OS Homo sapiens (Human).

CE Lutaryota; Metazoa; Chordata; Craniata; Vertebrata; Man

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RA RUBINSTEIN E., SERRU V., BOUCHEIX C.;

SUBSTITUTE CONTROL OF CONTROL OF CREATER CONTROL OF CONTROL O
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US-09-030-606-111 x 060745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 ATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCT
                                                                   GTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCCTCATCTTCATTGCTGAG
AAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGCTGT
                                                                                                                                                                                                                                                                                                                                                                    MetGlnCysPheSerPheIleLysThrMetMetIleLeuPheAsnLeuLe
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the EMBL/GenBank/DDBJ databases
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Gaps: 0
Percent Identity: 100.000
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72F5B872 CRC32;
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ae; Homo.
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sus scrofa (pig)
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alignment_scores:
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Ratio: 5.203
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                              US-09-030-606-111 x 060635
                                                                                                                                                      173 CATCTTTCTGTGTGGTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAA
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

TODD S.C., DOCTOR V.S., LEVY S.;

TODD S.C., DOCTOR V.S., LEVY S.;

SUBMITTED (MAR-1998) to the EMBL/GenBank/DDBJ databases

EMBL; AF054838; AAC69714.1; -.

PFAM; PF00335; transmembrane4; 1.

SEQUENCE 241 AA; 26302 MW; EF70913F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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273 ATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGT
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                                               MetGlnPheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValVa
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seq_documentation_block:
ID 075954
AC 075954;
AC 075954;
DT 01-NOV-1998 (TrEMBLrel 08
DT 01-NOV-1998 (TrEMBLrel 10
DE TETRASPAN NET-5.
OS HOMO Sapiens (Human).
OC Eukaryota; Metazoa; Chorda
OC Eutheria; Primates; Catarr
RN [1]
RP SEQUENCE FROM N.A.
RA RUBINSTEIN E., SERRU V., D
RT "New tetraspans identified
RL Submitted (SEP-1998) to th
DR EMBL; AF089749; AAC35859.1
DR PFAM; PF00335; transmembra
DR PROSITE; PS00421; TM4; 1.
SQ SEQUENCE 239 AA; 26779;
                                   alignment_scores:
Quality:
Ratio:
Percent Similarity:
alignment_block:
US-09-030-606-111 x 075954
                                                                                                                                                                                                                                                                                                                                                            seq_name: sp_human:075954
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                          SEQUENCE FROM N.A.

RUBINSTEIN E., SERRU V., DESSEN P., BOUCHEIX C.;

"New tetraspans identified in the EST database.";

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF089749; AAC35859.1; -.

EPAM; PF00335; transmebrane4; 1.

PROSITE; PS00421; TM4; 1.

SEQUENCE 239 AA; 26779 MW; 4CC44BFA CRC32;
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60.558
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                                     Gaps:
Identity:
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Align seg 1/1

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075954

from:

Н

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seq_documentation_block:
ID 070352 PRELIMINA
AC 070352;
DT 01-AUG-1998 (TrEMBLre
DT 01-AUG-1999 (TrEMBLre
DT 01-AWAY-1999 (TREMBLRE
DE METASTASIS SUPPRESSOR
                                                                                                                                                                                  seq_name: sp_rodent:070352
070352;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
METASTASIS SUPPRESSOR HOMOLOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 TCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCC
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                                                                                                                                                                                                                               H1s 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ......ValAsnGluAsnAlaLysLysAspLeuLysGluGlyLeuLeuL 125
                                                                                                                      PRELIMINARY;
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                                 update)
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SOR DREAM RECOGN
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Quality:
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Percent Similarity:
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Rattus norvegicus (Rat).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 TGCTTCAGCTTCATTAAGACCATGATGATCTCTTCAATTTGCTCATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUZUKI H., DONG J.T., GAO A.C., BARRETT J.C., Submitted (FEB-1998) to the EMBL/GenBank/DDBJ EMBL; AF049882; AACO5159.1; -
PFAM; PF00335; transmembrane4; 1.
PROSITE; PS00421; TM4; 1.
SEQUENCE 266 AA; 29487 MW; 9AlfE866 CRC32;
                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652 ACAAC....
                                                                                                            573 GGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAAAGAGAA 622
                                                                                                                                                                                                                             134 erSerArgGluGluAlaTrpAspTyrValGlnAlaGlnValLysCysCys 150
                                                                                                                                                                                                                                                                   523 AAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                 101 ThrValGluValLeuPheTyrPheAsnAlaAsnLysLeuLysGlnGluMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 CCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTGAGGTT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 GGCCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 TCTGTGTGCGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG
183 spAsnGlnLeuIleValLysLysGlyPheCysGluSerAspAsnSerThr
                                                                       166 nSerThrLysThrThrTyrProCysSerCysGluLysThrLysGluGluA
                                                                                                                                                                                                                                                                                                                                                                                                                       426 GCAGCTGCTGTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-KIDNEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 euLeuGlyLeuTyrPheValPheLeuLeuLeuIleLeuIleAlaGlnVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ...LeuGlnValGlyAlaTyrValPheIleGlyValGlyAlaIleThrMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 ysserSerPheIleSerValLeuGlnThrSerSerSerSer......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 CysValLysValThrLysTyrPheLeuPheLeuPheAsnLeuLeuPhePh
                                                                                                                                                  GlyTrpValSerProSerAsnTrpThrArgAsnProValLeuLys...As
                                                                                                                                                                                                                                                                                                                                          GACGTTGCTGGTAGTGCCTGCCATCAAGAAA...GATTATGGTTCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tLeuMetGlyPheLeuGlyCysIleGlyAlaValAsnGluValArgCysL
                                                                                                                                                                                                                                                                                                        tGlyAsnThrValMetAspIleIleGlnAsnTyrSerValAsnAlaSerS
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1.749
62.782
                                 ....GTCACCAACACAGCCAATGAAACC
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Gaps: 8
Percent Identity: 28.571
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alignment_block:
US-09-030-606-111 x 043657
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Quality:
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                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAEDA K., MATSUHASHI Y.;
"The CDNA cloning of a novel gene A15 homologue which encords a member of the transmembrane 4 superfamily ";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF043906; AAC64257.1; -.
EMBL; AF0439453; AAC642570.1; -.
EMBL; BABS; AAD00560.1; -.
EMBL; BABS; BAD00560.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T245 OR TSPAN-6.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200
  SEQUENCE FROM N.A.
TODD S.C., DOCTOR V.S.,
Submitted (MAR-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T245 PROTEIN
                                                                                                                           122 CATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAEDA K., MATSUHASI S., HORI K., XIN Z., MUKAI T., TABUCHI K., EGASHIRA M., NISHIKAWA N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
27
                                                                                    13 lileThrCysPhe.....LysSerValLeuLeuIleTyrThrPheI
                                                                                                                                                                                                     72 GCAGTTCCCTCTTTCAGAACTCACTGCCAAGAGCCCTGAACAGGAGCCAC
                                                                                                                                                                 2 AlaSerProSerArgArgLeuGln......ThrLysProVa 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCACCAAGCAAAAGGCTCACGACCAAAAAGTA.....GAGGGTTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCTGCCACTAC 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCAGCTGGAATTGGGGGCCTCGAGCTGGCTGCCATGATTGTGTCCATG 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tGluLysAlaGlnAlaTrpLeuGlnGluAsnPheGlyIleLeuLeuGlyV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_human:043657
                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 AA; 27563 MW;
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                                                                                                                                                                                                                                                                                                                                                    282.00
1.730
62.452
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. 06, Last sequence 10, Last annotation.
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the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                      Percent
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.
1E7E5802 CRC32;
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: Identity:
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RAP RAPA
                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID Q19983 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: sp_invertebrate:Q19983
                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL 01, 01-NOV-1996 (TREMBLREL 01, 01-MAY-1999 (TREMBLREL 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
SEQUENCE FROM N.A. MEDLINE; 94150718. WILSON R., AINSCOUGH
                                                                                                      SEQUENCE FROM N.A. PERCY C.;
                                                                                                                                                              Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhak
                                                                                                                                                                                                      Caenorhabditis elegans
                                                                                                                                                                                                                             F33C8.3
                                                                                                                                                                                                                                              F33C8.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                               Q19983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372
                                                                                 Submitted (FEB-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 CATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 ATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGACTTC.....ACTCAAGTGTGGAACACCATGAA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGCCATGATTGTGTCCATGTATCTGTACTGC 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpMetLeuLysLeuTyrAlaMetPheLeuThrLeuValPheLeuValG1 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCACCAACACAGCCAATGAAACCTGCACCAAGCAAAAGGCTCACGACCA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snTyrTyrSerGlu...LysGlyPheProLysSerCysCysLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTACTTCAAAGAGAACAGTGCCTTTCCCCCCATTCTGTTGCAATGACAAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ....LeuHisCysCysGlyValThrAspTyrArgAspTrpThrAspThrA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCAC 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAspTyrArgSerHisAlaValAspLysIleGlnAsnThr.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAAAGATTATGGTTCCCAG 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uLeuValAlaAlaIleValGlyPheValPheArgHisGluIleLysAsnS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTGCAGCTGCTGGTCGCCCTTGGTGTACACCACAATGGCTGAGCACT 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leIleLeuLeuGlyThrPheGlyCysPheAlaThrCysArgAlaSerAla
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    ANDERSON
                                                                                                                                                              oda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
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    BERKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
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alignment_scores:
Quality:
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US-09-030-606-111 x Q19983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: Q19983 from: 1 to: 282
                                                                                                                                                                                                                 479
                                                                                                                                                                                                                                        103
                                                                                                                                                                                                                                                                                                                                           329 TCTTGGTTTCCTGGGCTGCTATGGTGCCTAAGACTGAGAGCAAGTGTGCCC 378
:::|||:::::|||||||
69 uValGlyTyrPheGlyCysIleGlyAlaTrpLysMetAsnGlnCysAlaL 86
                                                                                                                                  136
                                                                                                                                                       529 TCACTCAAGTGTGGAACACCACCATGAAAGGGGCTCAAGTGCTGTGGCTTC 578
                                                                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                                                129 TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT 178
 625 GIGCCITI......
                           169
                                                                              153
                                                                                                                                                                                                                                                                 429 GCTGCTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCTGAC 478
                                                                                                                                                                                                                                                                                                      379 TCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTGAGGTTGCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 GGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TCTGTGTGGGGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG 228
                                                                                                                                                                                                                                                                                          37 roAlaAla...SerAspPhePheAlaLeuHisSerThrHisProGlyAla 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 pLeuSerGlyValValValPheGlyLeuGlyIleTrpLeuLeuPheAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAACTATACGGATTTT.....GAGGACTCACC 607
                                                                                                                                                                                    uSerSerMetTyrAspThrIleArgAsnArgTyrSerSerGluThrAlaP
                                                                                                                                                                                                              GTTGCTGGTAGTGCCTGCCATCAAGAAAGATTATGGTTCCCAGGAAGACT 528
                                                                                                                                                                                                                                        AlaAlaValThrLeuPheHisLysGlnGluHisIleLysHisTyrValGl 119
                          rGlnLeuGluValAsnGluGluAspAlaGlyArgIleGluHisGlyIleG 186
                                                    CTACTTCAAAGAGAAC.....A 624
                                                                                                                                heLysAspAlaPheAspThrValGlnGluLysPheGluCysCysGlyVal 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
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1.681
55.442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 294
Gaps: 6
Percent Identity: 24.830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.
6036A5B2 CRC32;
CCCCCATTC 641
                                                                                                                                                                                     136
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86 lyAlaPheGlyGlyAsnLysGlyThrGlyTyrGlyArgValProSerSer 2
642 TGTTGCAATGACAAGGTCACCAACAC 667 :::
CACCAAGCAAAAGGCTCACGACCAAA
8 GTTGCTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGTCACCGTG
::: :::::::::::::::::::::::::::
768 GGTGGTGTGGCAGCTGGAATTGGGGGCCTCGAGCTGGCTG
818 GTCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCTGCC 867 :
868 ACTACTGCCACATGGGAACTGTGAAGAGG 899
seq_name: sp_rodent:088429
q_documentation_block: O88429 PRELIMINARY O88429;
1998 (Tremb 1998 (Tremb 1999 (Tremb 1999 (Tremb RFACE GLYCO
Eutheria; Rodentia; S [1] SEQUENCE FROM N.A. STRAIN=C57BL/B6; TISS
HOSOKAWA Y., SENBA E. "Molecular cloning of transmembrane 4 super
neurons."; Submitted (MAR-1998) to the EMBL/GenBank/DDB EMBL, AR052492; AAC24579.1; PFAM; PF00335; transmembrane4; 1.
ignment_scores: Quality: 270.50 Length: 24
R Percent Simila
S-09-030-606-111 x 088429
seg 1/1 to: 088429 from: 1 to: 244
120 ACCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTT 169 3 ThrLysProValIleThrCysLeuLysThrLeuLeuIleIleTyrSerPh 19
170 GCTCATCTTTCTGTGTGGTGCÄGCCCTGTTGGCAGTGGGCATCTGGGTGT 219 ::::::::::::::::::::::::::::::::::::
220 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGT 269 :::::

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seq_documentation_block:
ID 070401;
AC 070401;
DT 01-AUG-1998 (TrEMBLTE
DT 01-AUG-1998 (TREMBLTE
DT 01-AVG-1999 (TREMBLTE
DT 01-MAY-1999 (TREMBLTE
DE TETRASPANIN TSPAN-6.
GN TSPAN-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; C
Eutheria; Rodentia; S
RN [1]
RP SEQUENCE FROM N.A.
RA TODD S.C., DOCTOR V.S
RA TODD S.C., DOCTOR V.S
RA SUDBILTED (MAR-1998)
DR EMBL; AF053454; AAAC69
DR PFAM; PF00335; transm
SQ SEQUENCE 245 AA; 2
alignment_scores:
Quality:
Ratio:
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                                                                                                                    SEQUENCE FROM N.A.

TODD S.C., DOCTOR V.S., LEVY S.;

TODD S.C., DOCTOR V.S., LEVY S.;

Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF053454; AAC69711.1; -.

PFAM; PF00335; transmembrane4; 1.

SEQUENCE 245 AA; 27333 MW; DCAB7D8D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TIEMBLIE1. 07, Created)
01-AUG-1998 (TIEMBLIE1. 07, Last sequence update)
01-AUX-1999 (TIEMBLIE1. 10, Last annotation update)
TETRASPANIN TSPAN-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 etAsnGluThrAspCysAsnProLeuAspLeuHisAsnLeuThrValAla 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 CCAATGAAACC...TGCACCAAGCAAAAAGGCTCACGACCAAAAAAGTA... 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 AGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AlaThrLysValAsnGlnLysGlyCysTyrAspLeuValThrSerPheMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 CTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAAAGATTATGGTTCCC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 GAGGTTGCAGCTGCTGGTCGCCTTGGTGTACACCACAATGGCTGAGCA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 GGTCTTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGAACTAATGCAGTCACCGTGGGTGGTGGCAGCTGGAATTGGGGGCC 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACAGTGCCTTTCCCCCATTCTGTTGCAATGACAACGTCACCAACACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAAAGA 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snAspGluArgSerArgAlaValAspHisValGlnProSerLeuSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGC 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pThrPheLeuArgThrTyrThrAspAlaMet...GlnAsnTyrAsnGlyA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rIleValValPheGlyLeuPheGlyCysPheAlaThrCysArgGlySerP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erGlnLeuIleGlyMetLeuLeuAlaCysCysLeu 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAGCTGCCATGATTGTGTCCATGTATCTG 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......GAGGGTTGCTTCAATCAGCTTTTGTATGACAT 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CysGlyValGlnAsnTyrThrAsnTrpSerSerSerProTyrPheLeuAs 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluLeuValAlaGlyIleSerGlyPheValPheArgHisGluIleLysAs 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roTrpMetLeuLysLeuTyrAlaMetPheLeuSerLeuValPheLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
              270.00
1.709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
            Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
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            241
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       669
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seq_name: sp_human:060637
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US-09-030-606-111 x 070401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: 070401 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 65.560
                                                                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 heLeuAla.....TyrCys
                                                                                                                                                                                                                                                                     814 TTGTGTCCATGTATCTGTACTGC 836
                                                                                                                                                                                                                                                                                                                             211 lValAlaGlyIleSerPheGlyValAlaCysPheGlnLeuIleGlyIleP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 667 CAGCCAATGAAACCTGCACCAAGCAAAAGGCTCACGACCAA...AAAGTA 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617 AGAGAACAGTGCCTTTCCCCCCATTCTGTTGCAATGACAACGTCACCAACA 666
:||| ::::::||||||| |||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 CysCysGlyValThrAsnTyrGlyAspTrpLysGlyThrAsnTyrTyrSe 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 hrGlyAspTyrArgSerGluAlaValAspLysIleGlnSerThrLeuHis 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||::::::|||||||||:::|||:::::|||::::
| 104 || GluLeuValAlaAlaIIeValGlyPheValPheArgHisGluIleLysAs || 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGT 269
                                                                                                                                                                                                                                                                                                                                                                                     764 corecereorescaecrecaarresesseccresacrescreccarea 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           714 GAGGGTTGCTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGTCAC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 .....LeuGluGlyCysTyrProGlnArgAspAlaAspLysValAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 GAGGTTGCAGCTGCTGGTCGCCTTGGTGTACACCACAATGGCTGAGCA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 GETCTTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 GCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 lileIleLeuLeuGlyThrPheGlyCysPheAlaThrCysArgThrSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 Ala......ThrAsnValProPheValLeuIleGlyThrGlyThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 ysVal.....SerLeuGluAsnTyrPheSerLeuLeuAsnGluLys 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 ellePheTrpIleThrGlyValIleLeuLeuAlaValGlyIleTrpGlyL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerPheLysSerAsnTyrGluAsnAlaLeu...LysGluTyrAsnSerT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluGlyCysPheIleLysValMetThrThrIleGluSerGluMetGlyVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               laTrpMetLeuLysLeuTyrAlaMetPheLeuThrLeuIlePheLeuVal 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGAAGACTTC...ACTCAAGTGTGGAACACCACCATGAAAGGGCTCAAG 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAAAGATTATGGTTCCC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 28.631
                                                                                                                                                                                                             232
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6
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060637; 01-AUG-1998 (TrEMBLrel. 07,

Created) PRT;

SOR RAPROCES

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TODD S.C., DOCTOR V.S., LEVY S.;
Submilted (MAR-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF054840; AAC69716.1; -.
PFAM: PF00335; transmembrane4; 1.
SEQUENCE 253 AA; 28017 MW; 533AB6BE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                       664
                                                                               164
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                                                                                                                                                            148
                                                                                                                                                                                                                                    131 roAspAlaAlaSerArgAlaIleAspTyrValGlnArgGlnLeuHisCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 TCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 CATCTTTCTGTGTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 CAGTGC...TTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCT
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                                 ACACAGCCAATGAAACCTGCACCAAGCAAAAGGCTCAC.....GACCAA 707
                                                                                                                                                       CysClyIleHisAsnTyrSerAspTrpGluAsnThrAspTrpPheLysGl
                                                                                                                                                                                             TGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAAAGA 619
                                                                                                                                                                                                                                                                                                                     uValAspArgSerIleGlnLysValTyrLysThrTyrAsnGlyThrAsnP
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                                                                                                              G....AACAGTGCCTTTCCCCCATTCTGTTGCAATGACAACGTCACCA 663
                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTGCAGCTGCTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArgC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGT 322
                                                                            uThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSerA 181
                                                                                                                                                                                                                                                                              AAGAC...TTCACTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGC 569
                                                                                                                                                                                                                                                                                                                                                             CCTGACGTTGCTGGTAGTGCCTGCCATCAAGAAAGATTATGGTTCCCAGG 522
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annotation update
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SO DE RESERVA DE COMPTE DE
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US-09-030-606-111 x 089118
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Ratio:
Percent Similarity:
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O89118; O1-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PLATELET ENDOTHELIAL TETRASPAN ANTIGEN-3.
PETA3 OR PETA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITTER S., SELDIN M.F., ASHMAN L.K.; "Characterisation of the mouse homologue of CD151 (PETA-3/SFA-1); genomic structure, chromosomal localisation and identification of novel splice forms."; Biochim. Biophys. Acta 1398:75-85(1998).
EMBL; AF033620; AAC25952.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                     391 TCTTCATCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTC
                                                                                                                                                                                                                         141 ATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTTTCTGTGTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U89772; AAC25976.1; -. PFAM; PF00335; LTANSMENDIANE4; 1. PROSITE; PS00421; TM4; 1. SEQUENCE 253 AA; 28246 MW; C5
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uAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrI
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      98267146.
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Percent Identity:
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seq_documentation_block:
ID 060636
AC 060636:
PRELIMINARY;
AC 060636:
DT 01-AUG-1998 (TrEMBLrel. 07
DT 01-MAY-1999 (TREMBLrel. 10
DE TSPAN-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chorda
OC Eutheria; Primates; Catarr
RN [1]
RP SEQUENCE FROM N.A.
RA TODD S.C., DOCTOR V.S., LE
RA TODD S.C., DOCTOR V.S., LE
RA SEQUENCE (MAR-1998) to th
DR EMBL; AF054839; AAC69715.1
DR PFAM; PF00335; transmembra
SQ SEQUENCE 222 AA; 24425.
                                                                       alignment_block:
US-09-030-606-111 x 060636
                                                                                                                                                                          alignment_scores:
Quality:
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                                                                                                                                   Ratio:
Percent Similarity:
                           Align seg 1/1 to:
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

TODD S.C., DOCTOR V.S., LEVY S.;

TODD S.C., DOCTOR V.S., LEVY S.;

SUBMITTED (MAR-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF054839; AAC69715.1; -.

PFAM; PF00335; transmembrane4; 1.

SEQUENCE 222 AA; 24425 MW; BEC51E9D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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!!!!!| ::: |||||:::
!nValPheGlyMetIlePheThrCysCysLeuTyrArgSerLeuLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluHisTyr 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nGluHisLeuArgValIleGlyAlaValGlyIleGlyIleAlaCysValG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleTyrLysValGluGlyGlyCysIleThrLysLeuGluThrPheIleGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTCAAAGA 619
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seq_documentation_block:
D 062745 PRELIMINARY; PRT; 236 AA.
AC 062745;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLEAL. 10, Last annotation update)
DE TARGET OF THE ANTIPROLIFERATIVE ANTIBODY.
                                                                                                                                                                                         seq_name: sp_rodent:Q62745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 AGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTC
                                                                                                                                                                                                                                                                                        843 CAA 845
                                                                                                                                                                                                                                                                                                                                           199 lyLeuThrIlePheGlyMetIlePheSerMetValLeuCysCysAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 CGTTGTGGTCTTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 TCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCC.....
                                                                                                                                                                                                                                              216 Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     743 CATCCGAACTAATGCAGTCACCGTGGGTGGTGGCAGCTGGAATTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 AGTGCCATGCAGTTTGTCAACGTGGGC...TACTTCCTCATCGCAGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 LysSerProGluTyrPheTyrValGlyLeuTyrValLeuValGlyAlaGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysCysGlyLysGluSerSerGluGlnValGlnProThrCysProLysGlu
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alignment_block:
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GEISERT E.E., MURPHY T.P., IRWIN M.H., I
"A novel cell adhesion molecule, G-CAM,
Neurosci. Lett. 133:262-266(1991).

[2]
                                 462
                                                                                                420
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                                                                                                                                                                                                                                                                                                                                                                                                                             179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Astrocyte growth, reactivity, and the target of the antiproliferative antibody, TAPA.";
J. Neurosci. 16:5478-5487(1996).
EMBL: U19894; AAC53103.1; --
PFAM: PF00335; transmembrane4; 1.
PROSITE; PS00421; TM4; 1.
SEQUENCE 236 AA; 25888 MW; AD742C53 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY; TISSUE-CEREBRAL CORTEX; MEDLINE; 96346153.
GEISERT E.E., YANG L., IRWIN M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRWIN M.H., GEISERT E.E.;
"The upregulation of a glial cell surface antigen scar in the rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 121
                                                                105
                                                                                                                                                               370
                                                                                                                                                                                                                                                                                              270
                                                                                                                                                                                                                                                                                                                                                              229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurosci. Lett. 154:57-60(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
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                                                                                  GAGGTTGCAGCTGCTGGTGGTCGCCTTGGTGTACACCACAATG.......
                                                                                                                                                 AGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCT 419
                                                                                                                                                                                          lmetmetPheValGlyPheLeuGlyCysTyrGlyAlaIleGlnGluSerG 88
                                                                                                                                                                                                                                                                                                                                                       GGGCATCCTTTCTGAAGATCTTC.......GGGCCACTGTCGTCCAGT 269
                                                                                                                               lnCysLeuLeuGlyThrPhePheThrCysLeuValIleLeuPheAlaCys 104
                                                                                                                                                                                                              GGTCTTTGCTCTTGGTTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCA 369
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pLeuAlaGlyGlyValIleLeuGlyValAlaLeuTrpLeuArgHisAspP
                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGTGTGCGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysThrLysCysIleLysTyrLeuLeuPheValPheAsnPheValPheTr
sAspValLysGlnPheTyrAspGlnAlaLeuGlnGlnAlaValMetAspA
                                ....GCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAAAG
                                                              GluValAlaAlaGlyIleTrpGlyPheValAsnLysAspGlnIleAlaLy
                                                                                                                                                                                                                                                                                            GCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGT 319
                                                                                                                                                                                                                                                                                                                            roGlnThrThrLeuLeuTyrLeuGluLeuGlyAspLysProAlaPro
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1.666
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alignment_block:
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ID 055158 PRELIMINARY;
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                                                                                                                             Align seg 1/1 to: 055158
                                                                                                                                                             05-09-030-606-111 \times 055158
                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                          coagulopathy.";
J. Cell Biol. 141:267-280(1998).
EMBL; Y13275; CAA73724.1; -
PFAM; PF00335; transmembrane4; 1.
PROSITE; PS00421; TM4; 1.
                            191 AGCCCTGTTGGCAGTGGGCCATCTGG.....GTGTCAATCGATGGGGCCAT 234
                                                                                 141 ATTAAGACCATGATGATCCTCTCAATTTGCTCATCTTTCTGTGTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98198483
CLAAS C., SEITER (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TREMBLRE1. 06, 01-JUN-1998 (TREMBLRE1. 06, 01-MAY-1999 (TREMBLRE1. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 GGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508
                                                                                                                                                                                                                                                                                                                                                                                                         metastasis-associated tetraspanin molecule and consumption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BD IX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D6.1A PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                       LAAS C., SEITER S., CLAAS A., SAVELYEVA L., SCHWAB M., Association between the rat homologue of CO-029, a
   24
rLeuIleLeuGlyLeuAlaIleTrpLeuArgValSerLySAspGlyLySG
                                                            leuLysTyrSerMetPhePhePheAsnPheLeuPheTrpValCysGlyTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aIleValValAlaValIleMet......IlePheG
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                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                            235 AA;
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1.562
64.435
                                                                                                                                                                                                                                                                                                            25580 MW;
                                                                                                                              from: 1
                                                                                                                                                                                                              Percent Identity: 28
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                            E098640B CRC32;
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
TETRASPANIN-CD63 RECEPTOR.
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cydonium.";
Mol. Mar.,Biol. Biotechnol. 0:0-0(0).
                                          WIMMER W., BOEHM M., BATEL R., SCHATTON W., FILIC Z., MUELLER W.E.G.; "Initiation of aquaculture of sponges for their sustainable production of bioactive metabolites in an open system: Example Geodia
                                                                                                                                                    Geodia cydonium (Sponge).
Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Astrophorida; Geodiidae; Geodia.
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227 alLeuTyrCysGlnIle 232
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                                                                                                            EQUENCE FROM N.A
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Ratio: 1.503
Percent Similarity: 59.387
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SEQUENCE
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                  784 GAATTGGGGGCCTCGAGCTGGCTGCCATGATTGTGTCCATGTATCTGTAC 833
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                                                      eValAspPheLeuArgGluTyrGlnLeuValAlaGlyAlaIleGlyIleT
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                                                                                                                                  .....TyrThrAspGlyCysArgAspSerPh
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511 ATGGTTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGG 560	
122 pValLysGlnPheTyrAspGlnAlaLeuGlnGlnAlaValValAspAsp. 138	
06 ValAlaAlaGlyIleTrpGlyPheValAsnLysAspGlnIleAlaLysAs 12	
23 GTTGCAGCTGCTGGTGGTCGCCTTGGTGTACACCACAATG	
373 GTGCCCTCGTGACGTTCTTCTTCATCCTCCTCATCTTCATTCTTGAG 422	
323 CTTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGT 372 ::: ::	
276 CAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGT 322 :::	
229 GGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATG 275 ::::::::::::::::::::::::::::::::::::	
179 TCTGTGTGGTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATG 228	
129 TGCTTCAGCTTCAGTTAAGACCATGATGATCCTCTTCAATTTGCTCATCTT 178 :: :::::::: ::::::::::	
Align seg 1/1 to: 097703 from: 1 to: 236	_
allgnment_block: US-09-030-606-111 x 097703	ع ۾
allgnment_scores: Quality: 228.50 Ratio: 1.554 Percent Similarity: 59.514 Percent Identity: 29.150	
□ 3 3 C > □ □	8222322
OS Cercopithecus aethiops (Green monkey) (Grivet). OS Cercopithecus aethiops (Green monkey) (Grivet). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; OC Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; OC Chlorocebus. RN [1]	2888
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eq_name: sp_mammal:09770	98
235CysLeuCys 237	
CICIO	
219 hrPheAiaVailleGinileAiaVaiVaiLeuileSerileVaiLeu 234	

139	AspAlaAsnAsnAlaLysAlaValLysThrPheHisGluThr 153	53
561	CTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCCTA	610
154	LeuAspCysCysGlySerSerThrLeuAlaAlaLeuThrThrSerVa 169	69
611	AGTGCCTTTCCCCCATTCTGTTGC	56
169	LeuLysAsnAsnLeuCysProSerGlySerAsnI 181	.81
657	AGCCAATGAAACCTGCACCAAGCAAAAAGGCTCACGAC	704
181	leIleSerAsnLeuLeuLysLysAspCys	191
705	CAAAAAGTAGAGGGTTGCTTCAATCAGCTTTTGTATGACATCCGAACTAA 754	54
192	GlnLysIleAspGluLeuPheSerGlyLysLeuTyrLeuIleGlyIleAl	208
755		804
208	aAlaIleValValAlavalIleMetileP	218
805	805 CTGCCATGATTGTGTCCATGTATCTGTACTGCAATCTACAA 845	
218	218 heGluMetIleLeuSerMetValLeuCysCysGlyIleArg 231	

Run

97.

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Title:
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ALIGNMENTS

Seguence	DEFINITION we68d03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346245 3' similar to TR:060635 060635 TSPAN-1. [1] ;, mRNA	AI660579/c
	mo sapiens cDNA clone 5 TSPAN-1. [1] ;, mRNA	10-MAY-1999

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                  TGGGAACTGTGAAGAGGCACCCTGGCAAGCAGCAGTGATTGGGGGAGGGGACAGGATCTA
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Email: Robert_Strausberg@nih.gov
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index.
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1 (bases 1 to 697)
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/db_xref="taxon:9606"
/map="between D11S1765 and UGB"
/clone="TMAGE:3346245"
/clone_11b="Soares_Dieckgraefe_colon_NHCD"
/tissue_type="colonic mucosa from 3 patient disease"
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On May 8, 1995 this
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1 (bases 1 to 593)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Chisque, T., Lacy, M., Le, M., Le, N., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA100799 593 bp mRNA
zm26d01.s1 Stratagene pancreas
IMAGE:526753 3', mRNA sequence
                                This clone is available royalty-free through LLNL : IMAGE Consortium (info@image.llnl.gov) for further Seq primer: -40M13 fwd. from Amersham
                                                                                                 Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                           4444 Forest Park Parkway,
                                                                                                                                                                                                                                           Washington University
                                                                                                                                                                                                                                                               Contact: Wilson RK
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                quality sequence stop: 353.
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/organism="Homo sapiens' /db_xref="GDB:3918182"

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                                                                                                                                                                                                                                                             GAGAGAAAGGCATTTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATG 1231
                                                                                                                                                                                                                                                                                   TATTAAACCCTTGATATGCCCCCTAGGCCTAGTGGTGATCCCAGTGCTCTACTGGGGGAT
                                                                                                                                                                                                                                                                                                          TATTAAACCCTTGATATGCCCCCTAGGCCTAGTGGTGATCCCAGTGCTCTACTGGGGGAT 1171
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                                                                                                      AI708181 557 bp mRNA EST 04-JUN as89f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335911 3' similar to TR:060635 060635 TSPAN-1. [1
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                   sequence.
AI708181
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No. 1.1e-141;
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 CTAAGGTAGCCAGTTCTGTTGCCCCATTCCCCCAGTCTATTAAACCCCTTGATATGCCCCCCT
                                                                                                                                                                                                           AGGCACCCTGGCAAGCAGCAGTGATTGGGGGGAGGGGGACAGGATCTAACAATGTCACTTGG
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                                                                                                                                                                           AGGCACCCTGGCAAGCAGCAGTGATTGGGGGGA-GGGACAGGATCTAACAATGTCACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 557)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU.NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
On Dec 20, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Possible reversed clone: similarity on Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult, age 25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Barstead colon HPLRB7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="19"
/clone="IMAGE:2335911"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 518; DB 51;
Pred. No. 3.7e-134;
0; Mismatches 10;
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|AAACCTGTTACAATGTTA 1
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1 (bases 1 to 562)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost, Skrizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189085.
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Email: est@watson.wustl.edu

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/clone="IMAGE:2334598"
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Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pAMP10; Site_1: Not1; Site_2: Economic cDNA was primed with oligo(dT)17 on 50 m DNAse-treated, total cellular RNA obtained from
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                  854 CTTCTGCCTCTGCCACTACTGCCACATGGGAACTGTGAAGAGGCACCCTGGCAAGCA 913
                                                                 CCTCGAGCTGGCCATGATTGTGTCCATGTATCTGTACTGCAATCTACAATAAGTCCA 420
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nc63b06.rl NCI_CGAP_Pr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)
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High quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: -28ml3 revl ET from Amersham quality sequence stop: 390.
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                        /note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of FCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:5923237"
/db_xref="taxon:9606"
/clone="IMAGE:745907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Prl"
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                                                                                                                                                                            37.0%;
99.8%;
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                                                                                                                                                                            Score 477.4; DB 33; Pred. No. 7.4e-123;
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AUTHORS
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AA468417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGTGATTGGGGGAGGGGACAGGATCTAACAATGTCACTTGGGCCAGAATGGACCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGCCTCTGGGTGGATGTGTAGAAGGCACTTCAAAATGCATAAACCTGTTACAATGTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGCCTCTGGGTGGATGTGTAGAAGGCACTTCAAAATGCATAAACCTTGTTACAATGTT 1272
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                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Warston Linehan, M.D., Rodrigo Chuaqu
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, P
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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AA468417
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                        Insert Length: 703 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 442.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
On Sep 12, 1996 this sequence version
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nc78e09.rl NCI_CGAP_Pr2 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (301) 496-1550
/dev_stage="45 years old"
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/note="Vector: pAMP10; Site_1tholigo(dT)17 on 50
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/sex="Male"
                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:783496"
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KEYWORDS SOURCE ORGANISM

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VERSION ACCESSION DEFINITION

AA593864.1 mRNA sequence. AA593864 g2408542

RESULT 8 AA593864/c

AA593864 470 bp mn19f08.sl NCI_CGAP_Col2

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Homo sapiens cDNA clone IMAGE:1084359

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REFERENCE AUTHORS

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 470)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy

Vertebrata;

Project (CGAP)

TITLE JOURNAL

Unpublished (1997)

Tumor Gene Index

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COUNT
               109
5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
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Query Match
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Matches 491
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                                                 CCCTTGATATGCCCCCTAGGCCTAGTGGTGATCCCAGTGCTCTACTGGGGGATGAGAGAA 1178
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                                                                                                       TCTAACAATGTCACTTGGGCCAGAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGCCTAG
                                                                                                                                                                                                                                                                              CACATGGGAACTGTGAAGAGGCACCCTGGCAAGCAGCAGTGATTGGGGGAGGGGACAGGA 938
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                                                                                                                               GGGGCATTCCAGAGCCTCTAAGGTAGCCAGTTCTGTTGCCCATTCCCCCAGTCTATTAAA 1118
                                                                                                                                                                                                               TCTAACAATGTCACTTGGGCCAGAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGCCTAG
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ilarity 98.2%;
Conservative
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Matches 469
                                                                                                                                                                                                                                                                                                                                                                1103 CCCCCAGTCTATTAAACCCCTTGATATGCCCCCTAGGCCTAGTGGTGATCCCAGTGCTCTA 1162
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                                                                                                                                                                                                                                                                                                                                    170
                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 GTGGGTGGATGGGTGGGGGCATTCCAGAGCCTCTAAGGTAGCCAGTTCTGTTGCCCATT 171
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                                                                       50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGACTTGGGGCTAGATAGGGACCACTCCTTTNAGCGATGCCTGACTTTCCTTCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGACTTGGGGCTAGATAGGGACCACTCCTTTT-AGCGATGCCTGACTTTCCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGTGGATGTGTAGAAGGCACTTCAAAATGCATAAACCTGTTACAATGTT 1272
                                                                                                                                                                                                CTGGGGGATGAGAGAAAGGCATTTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCT
                                                                                                                                                                                                                                                                                                                              CCCCCAGTCTATTAAACCCTTGATATGCCCCCCTAGGCCTAGTGGTGATCCCCAGTGCTCTA 111
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: L. J
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     음
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Seq primer: ~40ml3 fwd. ET from Amersham
High quality sequence stop: 435.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="colon tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: colon; Vector: Bluescript Sk-; Site_1:
/note="Organ: colon; Vector: Bluescript Sk-; Site_1:
/note="Organ: colon; Vector: Bluescript Sk-; Site_1:
/note="Organ: Solon tumors: 5" adaptor sequence: 5"
/
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/db_xref="taxon:9606"
/clone="IMAGE:1084359"
/clone_lib="NCI_CGAP_Co12"
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99.8%;
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Pred. No. 1.9e-117;
0; Mismatches 0;
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ORGANISM
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LOCUS
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                                                                    Query Match
Best Local Similarity
                                                    Matches 480;
790 GGGGCCTCGAGCTGGCCATGATTGTGTCCATGTATCTGTACTG-CAATCTACAATAA 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasce, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1834 Std Error: 0.00 Seq primer: -40Ml3 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97044478
On Sep 21, 1992 this
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1 (bases 1 to 488)
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IMAGE:376003
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                                                                                                                                                              123
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 434.
                                                                                                                                                                                      6 488 bp mRNA EST 01-FEB-1997
.sl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 76003 3', mRNA sequence.
                                                                                                                                                              NbHL19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/map="19p12-p13.1"
/clone="IMAGE:376003"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:1284259"
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                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="unknown"
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                                                                   35.4%;
99.0%;
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                                                Score 456.8; DB 27; Pred. No. 4.2e-117; 0; Mismatches 3;
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849 GTCCACTTCTGCCTGCCACTACTGCCACATGGGAACTGTGAAGAGGCACCCTGGC

908

GGGCCTNCGAGCTGCCATGATTGTGTCCATGTATCTGTACTGCCAATCTACAATAA 429

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REFERENCE
AUTHORS
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AA846269
                                                                                                                          Seq
                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 446)
                                                                                                                                        Insert Length: 1547
                                                                                                                                                                               cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                  www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                       Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                           primer:
                                                                                              primer: -40ml3 fwd. ET from quality sequence stop: 437. Location/Qualifiers
                                                                                                                                                                                                                                                    l: Robert_Strausberg@nih.gov
Library Preparation: M. Bento Soares,
/map="672C09; 17; 17p11.2; 21q"
/clone="IMAGE:1387451"
/clone_11b="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid_tumor"
                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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 REFERENCE
AUTHORS
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Query Match
Best Local Similarity
Matches 445; Conserv
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                                                                                                                                                                                                                                                                                                                       AAACCTGTTACAATGTTAAAAAAAA
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Eukaryota; Metazoa; (Eutheria; Primates; Calleria; Primates; Calleria; Louis 1 (bases 1 to 450)
NCI-CGAP http://www.r
                                                                                                                                                                     mRNA sequence.
AI075023
                                                                                                                                                                                                   AI075023 450 bp mRNA oq97h07.x1 NCI_CGAP_Co12 Homo
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                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DBIOB (ampicillin resistant)"
/not="DBIOB (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pT7T3D
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1:
Site_2: Eco RI; Ist strand cDNA was primed with
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                                      Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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Pred. No. 1.2e-113;
0; Mismatches 1;
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IMAGE:1594333
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                                   1243
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                                                                                      ATTTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAGGCA 1242
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                                   CTTCAAAATGCATAAACCTGTTACAATGTT 1272
                                                                                                                                                                                                               CATTCCAGAGCCTCTAAGGTAGCCAGTTCTGTTGCCCCATTCCCCCAGTCTATTAAACCCT
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                                                                                                                                          TGATATGCCCCCTAGGCCTAGTGGTGATCCCAGTGCTCTACTGGGGGGATGAGAGAAAGGC
                                                                     ATTTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAGGCA
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Unpublished (1997)
On Jan 17, 1998 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: L. Jeffrey Medeiros, M.D., Mi
Emmert Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 1215 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1594333"
/clone=1ib="NCI_CGAP_Co12"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="colon tumor"
/tissue_type="colon tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: colon; Vector: Bluescript SK-; Site_1:
/note="Organ: colon; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled colon tumors. 5' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTT 3' Average insert size: 1.2 kb.
a 123 c 109 g 104 t
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Pred. No. 7.1e-112;
0; Mismatches 0;
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AUTHORS
TITLE
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ORGANISM
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                               801 CTGGCTGCCATGATTGTGTCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGC 860
              62 CTGGCTGCCATGATTGTGTCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGC
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Query Match
Local Similarity nes 443; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linchan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found, through the I.M.A.G.E. Consortium/LLNL at:
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1 (bases 1 to 453)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA)

Tumor Gene Index
Unpublished (1997)

On May 8, 1995 this sequence version replaced gi:801529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar to
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                                                                                                      Conservative
                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                   /note="vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells
histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                           David Krizman
1 113 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:1203155"
/clone_11b="NCI_CGAP_Pr3"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 NCI_CGAP_Pr3
5 contains Alu
                                                                                                                             33.9%;
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                                                                                                   Score 437.6; DB 36
Pred. No. 9.2e-112;
0; Mismatches 9;
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                                                                                                                                                       DB 36;
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                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lini.gov/bbrp/image/image.html
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AA534171
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On Nov 29, 1993 this sequence version
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 496)
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National Cancer Institute, Cancer Genome Anatomy
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Location/Qualifiers
note—"Organ: prostate; Vector: pAMP10; mRNA made from invasive prostate tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman,
                                                                             /tissue_type="invasive prostate tumor"
/lab_host="DH10B"
                                                                                                                 /clone_lib="NCI_CGAP_Pr10"
/sex="male"
                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:997813"
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3', mRNA sequence.
AA861869
                                                                                          rel: (301) 496-1550
Email: Robert C
                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 456)
                                                                              Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento
           CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                       GGCATTTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAG
                                                                                                                                                                                                                     CCTTGATATGCCCCCTAGGCCTAGTGGTGATCCCAGTGCTCTACTGGGGGGATGAGAGAAA 1179
                                                                                                                                                                                                                                                               GGCATTTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAG
                                                                                                                                                                                                                                                                                     GGGCATTCCAGAGCCTCTAAGGTAGCCAGTTCTGTTGCCCCATTCCCCCAGTCTATTAAAC
                                                                                                                                                                                                                                                                                                           TAACAATGTCACTTGGGCCAGAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGCTAGAT
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Seq primer: -4(
                                            AI568832 440 bp mth16906.x1 NCI_CGAP_Pr28mRNA sequence.
            EST
                       g4532206
AI568832.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rt Length: 2340 Std Error: 0.00 primer: -40ml3 fwd. ET from Amersham quality sequence stop: 431.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD)
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1408786"
/clone_lib="Soares_testis_NHT"
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99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 431.4; DB 39;
Pred. No. 4.9e-110;
O; Mismatches 1;
                                                                   Homo
                                                                   sapiens cDNA clone
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IMAGE:2118490 3',
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Best Local S
Matches 439
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TITLE
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Homo sapiens
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1134 CTAGGCCTAGTGGTGATCCCAGTGCTCTACTGGGGGATGAGAGAAAAGGCATTTTATAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 GCAATCTACAATAAGTCCACTTCTGCCTCTGCCACTACTGCTGCCACATGGGAACTGTGA 381
                                                                                                                                                                                                                                                                             GGGCCAGAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGGCTAGATAGGGACCACTCCTT 1014
                                                                         CTCTAAGGTAGCCAGTTCTGTTGCCCATTCCCCCCAGTCTATTAAACCCCTTGATATGCCCC 1133
                                                                                                                                                                           AGAGGCACCCTGGCAAGCAGTGATTGGGGGAGGGGACAGGATCTAACAATGTCACTT 954
                                               CTCTAAGGTAGCCAGTTCTGTTGCCCATTCCCCCAGTCTATTAAACCCTTGATATGCCCC
                                                                                                                                                   GGGCCAGAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGGCTAGATAGGGACCACTCCTT
                                                                                                                                                                                                                                                                                                                                                    AGAGGCACCCTGGCAAGCAGCAGTGATTGGGGGGAGGGGACAGGATCTAACAATGTCACTT 321
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. B:
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Feb 18, 1999
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National Cancer Institute, Cancer Genome Anatomy
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Seq primer: -40UP f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.

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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Pr28"
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Pred. No. 4.3e-109;
0; Mismatches 0;
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1408.299 Million cell updates/sec
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Result No.

Score 1266

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AF065388

Description

Query Match Length DB

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AF065388 Homo sapi REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE VERSION
KEYWORDS
SOURCE
ORGANISM ACCESSION RESULT AF065388 UIN FEATURES COCUS JOURNAL source 81.8 73.2 772.2 771.6 662.8 662.8 660.4 660.4 7.5 9 Homo sapiens AF065388 g3152700 AF065388.1 G 2 (bases 1 to 1278)
3 (bases 1 to 1278)
5 (bases 1 to 1278)
6 (bases 1 to 1278)
7 (bas Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1278)

Rubinstein,E., Serru,V. and Boucheix,C.

New tetraspans identified in the EST database

Unpublished Homo sapiens AF065388 numan . /organism="Homo sapiens" GI:3152700 1076 849 1358 1432 1432 1720 1720 1278 bp tetraspan HUMCD63
HUMCGCB
0 HSME491
0 HSR2IMP
0 S48196
0 S93788
1 HSU20770
RABME491CD
2 MUSCD9ANT
2 MMCSCCD53 HUMTAPA1

MUSTALLA

AF116600

AF116599

HUMCD53

HUMCD53GLY

RNU19894

HUMA15 HUMTALLA1 MMMD3MRN AR016441 E05732 MUSC33R2IA AR016440 HUMP24CD9A HSMRP1 MMIGCD53A DMC8D8 AF049882 CELC14A11 AF054839 D89290 MMU89772 I13743 I13744 HUMMRNAB HUMANTCD9 AGMDRAP27 RATOX44 mRNA NET-1 ALIGNMENTS mRNA, complete cds. AF054838 Homo sapi AF054841 Homo sapi AF025413 Homo sapi AF089749 Homo sapi AF089749 Homo sapi AF089749 Mus muscu M33680 Human 26-kD D26483 Mouse mRNA AF116599 Chloroceb M60871 Human CD53 U19894 Rattus norv D10653 Homo sapien L10373 Human (Clon D29808 Human mRNA X59047 M.musculus M57276 Rat leukocy D14883 Mouse mRNA AR016440 Sequence E05732 CDNA encodi I13743 Sequence 2 D113744 Sequence 3 D10726 AR1can gre L34068 Human mrla X690111 H.sapiens m M38690 Human melan X63795 Human R2 mR S48196 C33 antigen S9395 Human melan X63795 Human melan L08115 Mus musculu X97227 M.musculus Z16071 Mus musculu AL022018 Drosophii AF049882 Rattus no U97592 Caenorhabdi AF054839 Homo sapi D89290 Mus musculu U89772 Mus musculu 25-MAY-1998

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SPYFKENSAF PPFCCNDMYTNTANETCTKQKAHDQKVEGCFNQLLYDIKTNAVTVGGV
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AF054838.1 G.
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Todd, S.C., Doctor, V.S. and Levy, S.
                                                                                                                                                                                                                        Sequences and expression tetraspanin/TM4SF family
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/gene="TSPAN-1"
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              GCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATGGGGCATCCTTTCTGAAGATC
                                                                  TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTTTCTGTGTGGT 188
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TGTGGCGTGCTGGGTGTCGGCATCTGGCT----
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Homo sapiens
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g2997746
AF054841.1 G
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1 (bases 1 to 849)

Todd,S.C., Doctor,V.S. and Levy,S.

Sequences and expression of six new members of the tetraspanin/TM4SF family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-MAR-1998)
CA 94305-5115, USA
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Todd, S.C., Doctor, V.S.
Direct Submission
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                                                                                                                     Similarity
                                                                                                                                                                                         132
                                                                                                        Conservative
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                                                                                                                                                                                     /product-"terraspan TM4SF"
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/product-"terraspan TM4SF"
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NATRVPDSCCLEFSESCGLHAPGTWWKAPCYETVKVWLQENLLAVGIFGLCTALVQIL
GLTFAMTMYCQVVKADTYCA"
a 284 c 249 g 184 t
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119. .835
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                     /gene="TSPAN-4"
/note="tetraspanin;
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92586349
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                                                                                                                                                                                                                                                                                                                                    Submitted (04-SEP-1997) Tumor Virology, Institute, 44 Binney Street, Boston, MA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAG-2, a novel transmembrane-4 superfamily (TM4SF) complexes with integrins and other TM4SF proteins J. Biol. Chem. 272 (46), 29181-29189 (1997)
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                                                                                                                                                                                                                                                                           /cell
                                                                                                                                                                                           /gene="NAG-2"
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                                                                                                                                                                                                                                                       cell
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Pell_line="MDA-MB-435"
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02115, USA
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AF089749
g3603458
                                                                                                                                                                                             Rubinstein, E., Serru, V., Dessen Direct Submission Submitted (01-SEP-1998) INSERM Villejuif 94807, France
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1432)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF089749
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/product="tetraspan NET-5"
/product="tetraspan NET-5"
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/db_xref="PID:93603459"
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/translation="MARGCLCCLKYMMFLFNLIFWLCGCGLLGVGIWLSVSQGNFATF
/Translation="MARGCLCCLKYMMFLFNLIFWLCGCGLLGVGIWLSVSQGNFATF
                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
127. .846
                                                                                                                                                                                 Location/Qualifiers
                                                                                         /codon_start=1
                                                                                                         /note="TM4SF; transmembrane
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                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 835)
Hosokawa, Y., Senba, E. and Seto, M.
Molecular cloning of a cDNA encoding mouse A15, a me transmembrane 4 superfamily and its preferential experience.
                                                                            Submitted (06-MAR-1998) Lab of Chemotherapy, A Research Institute, Kanakoden 1-1, Chikusa-ku,
                                                                                                                                                                                                                                                                                                                    Mus musculus
AF052492
                                                                                                                                             Unpublished
                                                                                                                                                         brain neurons
                                                                                                                                                                                                                                                                                                                                                AF052492
                                                                                                      Direct Submission
                                                                                                                                                                                                                                                      Mus musculus
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                                                                  464-8681,
                                                                                                                  Hosokawa, Y., Senba, E. and Seto, M.
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GENTVPDRCCMENSQGCGNATTPLWRTGCYEKVKMWFDDNKHVLGTVGMCILIMOIL
GMAFSWTLFGHHHRTGKKYDA"
3 410 c 405 g 321 t
/organism="Mus musculus"
/strain="C57BL/B6"
/db_xref="taxon:10090"
                                      Location/Qualifiers
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                                                                TGGAACACCACCATGAAAGGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGAG
                                                                                                                                                                                                                                                               TTGCTGGTAGTGCCTGCCATCAAGAAAGATTATGGTTCCCCAGGAAGACTTCACTCAAGTG
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TTTGGAATTGCGTTCTCCCAGTTGATTGGCATGCTGCTGGCTTGCTGTCTCTCCCG
                                                                                               TGCAATCCCCTGGATCTGCACAATCTGACTGTGGCCGCCACCAAAGTTAATCAGAAGGGC
                                                                                                                        ACCAACACAGCCAATGAAACCTGCACCAAGCAAAAAGGCTCACGACCAAAAAGTAGAGGGT
                                                                                                                                              AGCAGCCCCTACTTCCTGGACCATGGCATCCCCCCCAGTTGCTGCATGAACGAAACTGAC
                                                                                                                                                                      GACTCACCCTACTTCAAAGAGAACAGTGCCTTTCCCCCCATTCTGTTGCAATGACAACGTC
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                                               TGTTATGATCTGGTGACCAGTTTTATGGAGACTAACATGGGGATCATTGCTGGAGTGGCA
                                                                                                                                                                                                                                                AGGACTTACACGGATGCCATGCAGAACTACAATGG----CAATGATGAGAGGAGCCGGGCT
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6. .740
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/product="cell
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                                                                                                                                                                                                                                                          AAGATCTTCGGGCCACTGTCGTCCAGTGCCAGTTTGTCAACGTGGGCTACTTCCTC 302
                                                                                                                                                                                                                                                                                                                                                GGCGTGATCCTGGGTGTGGCCCTGTGGCTCCGCCATGACCCGCAGACCACCAACCTCCTG 373
                                             TTCTATGACCAGGCCCTACAGCAGGCCGTGGTGGATGATGACGCCAACAACGCCCAAGGCT 673
                                                                         CTGGTAGTGCCTGCCATCAAGAA-----AGATTATGGTTCCCAGGAAGACTTCACTCAA
                                                                                                        GTGGCCGCCGGCATCTGGGGGCTTTGTCAACAAGGACCAGATCGCCAAGGATGTGAAGCAG
                                                                                                                                     GTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCTGACGTTG 482
                                                                                                                                                                    GAATCCCAGTGCCTGCGGGACGTTCTTCACCTGCCTGGTCATCCTGTTTGCCTGTGAG
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90318365
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by S.I
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Human 26-kDa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MGVEGCTKCIKYLLEVENEVEWLAGGVILGVALWLRHDPQTTNL LYLELGDKPAPMTEYVGIYILIAVGAVMMEVGELGCYGAIQESQCLLGTEFTGLVILFACEVARAFOREGENIKOLGALQQAVVDDDANNAKAVVKTFHETLDCCGSSTLTALTTSVLKNNLCPSGSNIISNLEKEDCHQKIDDLESGKLYLIGIAAIVVAVIMIFEMILSMVLCGIRNSSVY"
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/db_xref="taxon:9606"
239. .949
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/db_xref="PID:g338678"
/db_xref="GI:338678"
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ACCAAACCTGTGATAACCTGTCTCAAAACCCTCCTCATCATCTACTCCTTCGTCTTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (11-JAN-1994) to the DDBJ/EMBL/GenBank databases. Izumi submitted (11-JAN-1994) to the DDBJ/EMBL/GenBank databases. Izumi Ishikawa, Shionogi Institute for Medical Science; 2-5-1 Mishima, Settsu, Osaka 566, Japan (Tel:06-382-2612(ex.478), Fax:06-382-2598)
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Mouse mRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagira, M., Ishikawa, I., Fujikawa, K., Molecular Cloning and Expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (strain:Balb/c) adult clone_lib:library of M.Nagira clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D26483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishikawa,I.
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(bases 1 to 1720)
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                                                             Conservative
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                                                                                                                                                                                                             /product="murine PE31/TALLA" 740. .1719
                                                                                                                                                                                                                                                                                           /translation="metrpvitclktlliiysfvfwitgvillavgvwgkltlgtyis
LIAENSTNAPYVLIGTGTTIVVFGLFGCFATCRGSPWMLKLYAMFLSLVFLAELVAGI
SGFVFRHEIKDTFLRTYTDAMQNYNGNDERSRAVDHVQRSLSCCGVQNYTNWSSSPYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="murine counterpart of Al5 (T-ALL associated
antigen) and CCG-B7 which is expressed in the brain
                                                                                                                                                                                                                                                                                                                                         /product="murine PE31 (TALLA)"
/protein_id="BAA05493.1"
/db_xref="PID:d1006037"
/db_xref="PID:g685221"
/db_xref="GI:685221"
                                                                                                                                                                                                                                                                                                                                                                                                                                           containing CCG triplet repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="library of M.Nagira"
/dev_stage="adult 8w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="Balb/c"
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/clone="MPE31-1"
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or PE31/TALLA,
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                                                                            Score 71.6;
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Pan troglodytes
AF116600
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AF116600.1
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 711)
Levy.S. and Kuo,C.C.
CD81 CDNA sequence derived from chimpanzee cells
                                                                                                    Submitted (24-DEC-1998)
                                                                                                                                                                                                                                                 chimpanzee
                                                                                                                              2 (bases 1 to 711)
Levy,S. and Kuo,C.C.
                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                      Pan troglodytes
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          /organism="Pan troglodytes"
/db_xref="taxon:9598"
/cell_line="Janice"
/note="EBV-transformed cells;
 CD81-derived
                                                                            Location/Qualifiers
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Chlorocebus :
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                                                                   African green monkey. Chlorocebus aethiops
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
 Levy,S.
                            Chlorocebus.
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Similarity 49.7%;
              (bases 1 to 711)
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 and Kuo, C.C
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LYLELGRKPAPWTFYVGLYILIAVGAVMMFVGFLGCYGALQESQCLLGTFFTCLVILF
ACEVAAGIWGFVNKDQJAKDVKOFYDDALQAVVDDDANMAKAVVKTFHETLDCGSS
TLTALITSVLKNNLCPSGSNIISNLFKEDCHQKIDDLFSGKLYLIGIAAIVVAVIMIF
EMILSWYLCCGIRNSVY"
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/codon_start=1
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/protein_id="AAD11440.1"
/db_xref="PID:g4206173"
/db_xref="GI:4206173"
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                                                                                                                                                                                                                                                                             GGAATCCCAGTGCCTGGGGGACGTTCTTCACCTGTCTGGTCATCCTGTTTGCCTGTGA 314
                                                                                                                                                                                                                                                                                                       TGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTGA 421
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                                                                                                                                                                                                                                                                                                                                                                                        GTATCTGGAGCTGGGAGACAAGCCTGCACCCAATACCTTCTACGTAGGCATCTACATCCT 194
                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTGGGCTACTTCCT 301
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                                                                                                            CGTGGTGAAGACCTTCCACGAGACGCTTGACTGCTGTGGCTCCAGCA
                                                                                                                                                                                                                        AGTGGCAGCCGGCATCTGGGGGCTTTGTCAACAAGGACCAGGATTGCCAAGGATGTGAAGCA 374
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              Human cell surface antigen (CD53) mRNA, M60871
·9160140
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Unpublished
                                         HUMCD53
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/db_xref="PID:g4206171"
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/db_xref="taxon:9534"
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No. 4.2e-09;
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Best Local Similarity 51.2%;
Matches 173; Conservative
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                                                                                                                                                                                                                                                                                                  GGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGC 496
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                                                                                                              ATTTCTGCAGTGTTGTGGTATAAATGGCACGAGTGATT
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1 (bases 1 to 1452)
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 HUMCD53GLY
Human CD53
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/db_xref="GDB:GO0-127-521"
/product="cell surface antig
/protein_id="AAA51951.1"
/db_xref="PID:g180141"
/db_xref="FID:g180141"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="promyelocytic
/map="Unassigned"
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Best Local Similarity 51.2%;
Matches 173; Conservative
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                                                                                                                                                                                             CATCAAGAAAGATTATGGTTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACCATGAA 556
                                                                                                                                                                                                                                                                                     GGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGC 496
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g180142
M37033.1
                                          RATTUS norvegicus
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1 (bases 1 to 1480)

Angelisova, P., Vlcek, C., Stefanova, I., Lipoldova, M. and Horejsi, V. The human leucocyte surface antigen CD53 is a protein structurally similar to the CD3 and MRC OX-44 antigens

Immunogenetics 32, 281-285 (1990)
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                               complete
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                                cds.
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/db_xref="taxon:9606"
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1 353 c
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HNLPSLTLGNVFVIVGSIHNVAFLGGMGSIKNKCLLMSFFILLLIILLAITLAS
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CPSDRKVEGCYAKARLWFHSNFLYIGIITICVCVIEVLGMSFALTLNCQIDKTSQTIG
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Pred. No. 1.3e-07;
0; Mismatches 162;
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TACCTGGAACTGGGAGACAAACCAGCACCTAGCACCTTCTATGTGGGCATCTACATTCTC
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Query Match 4.8%;
Best Local Similarity 53.5%;
Matches 177; Conservative
                                                                                 GCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATGGGGCATCCTTTCTGAAGATC 248
                                                                                                                                              TTCGGGCCACTG-----TCGTCCAGTGCCATGCAGTTTGTCAACGTG-GGCTACTTCCTC 302
                                                                                                                                                                                           TGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTTTCTGTGTGGT 188
                                             GGTGTGATCCTAGGTGTAGCTCTGTGGTTGCGCCATGATCCACAGACCACCACCTTGCTC 357
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1 (bases 1 to 1303)

Geisert, E.E. Jr., Murphy, T.P., Irwin, M.H. and Larjava, H.
A novel cell adhesion molecule, G-CAM, found on cultured rat
Neurosci. Lett. 133 (2), 262-266 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-JAN-1995) Eldon E. Geisert Jr., Department of Anatomy and Neurobiology, University of Tennessee, Memphis, 855 Monroe Ave., Memphis, TN 38163, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 (bases 1 to 1303)
Geisert, E.E.
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Geisert, E.E. Jr., Yang, L. and Irwin, M.
Astrocyte growth, reactivity, and the
antiproliferative antibody, TAPA
J. Neurosci. 16 (17), 5478-5487 (1996)
96346153
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Irwin,M.H. and Gelsert,E.E. Jr.

The upregulation of a glial cell surface
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Eutheria; Rodentia;
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lylelodkpabstryvgiyillavgavwmevgelgcygaigesocllgtetclvile

Acevaagiwgevukdgiakdvkgfydgalqqavmdddannakavvktfehetlnccgsn

Tlttltavlrnsicpsssnsetglikedchqkidelesgklyligiaaivvavimie

Emilsyvlccgirnssvy"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"target of the antiproliferative antibody"
/protein_id-"AAC53103.1"
/db_xref="PD:91142642"
/db_xref-"GI:1142642"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="1.1, sp1, sp2"
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/tissue_type="cerebral cortex"
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Pred. No. 1.9e-07;
0; Mismatches 148;
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g185900
g10653.1 GI:285900
ME491/CD63 superfamily; cell surface glycoprotein.
ME491/CD63 superfamily; cell lymphocyte cell_line:HPB-ALL
Homo sapiens immature T cell lymphocyte cell_line:HPB-ALL
mRNA, clone_lib:lambda gt10 clone:Al5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-FEB-1992) to the DDBJ/EMBL/GenBank databases. Nobuhlko Emi, Nagoya University School of Medicine, First Dept. of Internal Medicine; 65 Tsurumai, Showa-ku, Nagoya, Aichi 466, Japan (Tel:052-741-2111, Fax:052-741-1612)
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Isolation of a novel cDNA clone showing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ME491/CD63 superfamily Immunogenetics 37 (3), 193-198 (1993)
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                                                                                               /translation="metkpvitclktlliysfvfwitgvillavgvwgkltlgtyis
LIAENSTNAPYVLIGTGTTIVVFGLFGCFATCRGSPWMLKLYAMFLSLVFLAELVAGI
SGFVFFHEIKOTFLRTYTDAMOTYNGNDERSRAVDHVQRSLSCCGVQNYTNWSTSPYF
LEHGIPPSCCMNETDCNPQDLHNLTVAATKVNQKGCYDLVTSFMETNMGIIAGVAFGI
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                                                                                                                                                                                                        /codon_start=1
/product="cell surface glycoprotein"
/protein_id="BAA01501.1"
/db_xref="PID:d1001976"
                                                                                                                                                                                                                                                                                  /gene="A15"
25. .759
                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/cell_line="HPB-ALL"
                                                                                                                                                                               /db_xref="PID:g285901"
/db_xref="GI:285901"
                                                                                                                                                                                                                                                               /gene="A15"
                                                                                                                                                                                                                                                                                                            /tissue_type="immature T
                                                                                                                                                                                                                                                                                                                                      /clone_lib="lambda gt10"
                                                                                                                                                                                                                                                                                                                                                  /clone="A15"
                                                                                                                                                                                                                                                                                                                                                              /cell_type="lymphocyte"
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L10373.1
                                                 Genomics
93315145
                                                                                                                                                                                                                                                                                 Human
L10373
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1792)
Li,S.-H., McInnis,M., Margolis,R., Antonarakis,S. ar Novel triplet repeat containing genes in human brain expression, and length polymorphisms Genomics 16, 572-579 (1993)
                                                                                                                                                                               frontal Cort
Homo sapiens
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    1. .1792
    /organism="Homo sapiens"

                              Location/Qualifiers
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                                   780 GCTGGAATTGGGGGCCTCGAGCTGGCTGCCATGATTGTGTCCATGTATCTGTACTG 835
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/dev_stage="85 years"
/sex="female"
/sex="frontal Cortex"
/tissue_type="frontal Cortex"
/tissue_11b="Stratagene lambda ZAP II"
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27-AUG-1998.
25-FEB-1998; US-904809.
09-FEB-1997; US-806596.
01-AUG-1997; US-904809.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI, 98-480805/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers Claim 1; Page 85; 141pp; English.

This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers.

Sequence 1289 BP; 292 A; 335 C; 328 G; 334 T;
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V58587;
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                                              TGTGTGGTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATGGGGCATCCTTTC
CTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTG
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Scoring table: Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd

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06-JAN-1999 (first entry)
Full length cDNA sequence of prostate tumour clone N1-1862.
Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
Homo sapiens.
W09837093-A2.
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01-AUG-1997; US-9048
(CORI-) CORINA CORP
Dillon DC, Xu U,
WPI; 98-609886/51.
P-PSDB; W71870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 80; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itse can be used as a vaccine for the treatment of prostate cancer. The I was identified by analysis of a subtracted CDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.

Sequence 1289 BP; 292 A; 335 C; 328 G; 334 T;
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Human secreted pro
AR415_4; secreted
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Human secreted protein AR4
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437. .1162

/*tag= a

476. .514

/*tag= b

/note= "putative l

515. .1159
                                                                                              Location/Qualifiers
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                                                                                                                                           AR415_4 cDNA
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PS Claim i; Page 66-67; 114pp; English.
CC secreted protein (see W58380). It was isolated from a human adult cretina cDNA library using methods selective for cDNAs that encode cc secreted proteins. The clone is deposited in composite clone antigens. Novel cDNA clones (see V3933) is designed to isolate cthe clone from the composite. The predicted AT415_4 amino acid contidens. Novel cDNA clones (see V3933) is designed to isolate composite clone from the composite. The predicted AT415_4 amino acid contidens. Novel cDNA clones (see V39033) is designed to isolate clone from the composite. The predicted AT415_4 amino acid contidens. Novel cDNA clones (see V39033) is designed to isolate clone from the composite. The secreted proteins for analysis, cc characteristation, diagnostic or therapeutic use. They can also be used as tissue or moliwt markers, for chromosome identification, contentify genetic disorders, to isolate new related DNA, as sources of primers for PCR, to generate antibodies, and in contentify genetic disorders, to isolate new related DNA, as sources of primers for PCR, to generate antibodies, and in continification activity, chemotactic or chemokinetic activity, activing antibodies and thrombolytic activity, receptor/ligand activity, activing antibodies and thrombolytic activity, receptor/ligand activity, can also be continification activity. The proteins can be expressed in conform DNA, introduced in gene therapy vectors.

Sequence 1605 BP; 360 A; 427 C; 399 G; 419 T;
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Best Local Similarity
Matches 1287; Conser
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Racie LA, Spaulding V, Treacy M;
WPI; 98-261426/23.
P-PSDB: W58380.
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24-OCT-1997; US-740274.
25-OCT-1996; US-740274.
(GEMY) GENETICS INST INC.
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AGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCTGACGT
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                        GAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGCTAGATAGGGACCACTCCTTTTA-GC
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                                                                                                                                 GAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGGTAGATAGGGGACCACTCCTTTTAGGC
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POS KKKKKKK KE DO AC V34225 standard; DNA; 1324 BP.

V34225;

28-JAN-1999 (first entry)

Human secreted protein gene 4 clone HKCSR70.

Human; secreted protein; fusion protein; gene therapy; protein therapy; dalagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; inmune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoprosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens W09839446-A2

11-SEP-1998 06-MAR-1998 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 11-APR-1997 11-APR-1997 11-APR-1997 11-APR-1997 11-APR-1997 11-APR-1997 11-APR-1997

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PI Feng P, Ferrie AM, Fischer CL, Graves KA, Greene JM, Hu
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rose,
I Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeno P, R WPI; 98-60988751.
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                                                                                                                                                                                                                                                                                                                                            PT New isolated human genes and the secreted polypeptides they encode provides they encode provides for diagnosis and treatment of e.g. cancers, neurological provides for diagnosis and treatment of e.g. cancers, neurological provides for diagnosis and treatment of e.g. cancers, neurological provides for inflammation or blood disorders claim 1; page 226; 447pp; English.

Compared to the gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion compared to the human protein only.

Compared to the human protein only.

Compared to the human protein only.

Compared to the human protein only and their fragments (nucleic acid sequences: V34154-V34276; amino acid sequences W75057-W75179) which care useful for preventing, treating or ameliorating medical conditions can be considered by determining the amount of the new polypoptides in a sample cor by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 70 polynucleotides, based on which tissues they are most highly expressed in (see V34154 for described conservibles).
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Best Local Similarity 99.8%;
Matches 1273; Conservative
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 TGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTGGGCTACTTCC
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                                                          ATGCCTGACTTTCCTTCCATTGGTGGGTGGATGGGTGGGGGGCATTCCAGAGCCTCTAAG
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23-JUL-1998; U00959.
21-JAN-1997; US-034205.
21-JAN-1997; US-034204.
(HUMA-) HUMAN GENOME SCI INC.
Gentz RL, N1 J, Rosen CA;
WPI; 98-427559/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 36-37; 79pp; English.

Clone HPWARD5 is a member of the TMASF receptor superfamily. The products generated using the receptor can be used for treating abnormal conditions related to both an excess of and insufficient amounts of receptor activity. They can be used in the treatment of e.g. immune disorders, cancers, blood disorders, juvenile rheumatoid arthritis, Graves disease or immunocompromised disease states. The products can also be used for detection and diagnosis.

Sequence 1288 BP; 293 A; 333 C; 328 G; 334 T;
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V48113;
27-OCT-1998 (first entry)
Nucleotide sequence encoding clone HPWAE25
ds; human; receptor; immune disorder; cance
juvenile rheumatoid arthritis; Graves disea
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used to develop products for diagnosing or treating e.g. immune
isorders, cancers, blood disorders or immuno-compromised disease
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GTAGTGCCTGCCATCAAGAAAGATTATGGTTCCCAGGAAGACTTCACTCAAGTGTGGAAC
                                                    AGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTGAGGTT
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                                                                     v54014 standard; cDNA; 933 BP.
v54014;
02-DEC-1998 (first entry)
Nucleotide sequence of the human tumour-associated antigen.
Human; tumour-associated antigen; PRAT; stimulation; cell pantagonist; cancer; genetic defect; sickle cell anaemia; agantibody; hybridisation; probe; ss.
WO9838310-A1.
03-SEP-1998.
27-FEB-1998; U03953.
28-FEB-1997; US-808148
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Fig. Human fumour-associated antigen PRAT - useful for stimulating cell proliferation and screening for antagonists useful to treat or prevent cell proliferation disorders e.g. cancers S Disclosure; Fig la-1C; 54pp; English.

CC This is the nucleotide sequence of the human tumour-associated antigen CC (PRAT) used in the method of the invention for stimulating cell ccell proliferation and screening for antagonists useful to treat or prevent CC cell proliferation disorders such as cancer, and genetic defect e.g. csickle cell anaemia. The polypeptides can be combined with a suitable carrier in pharmaceutical compositions, and also used to screen for antagonists, agonists, and to generate antibodies. PRAT agonists can be added to a cell to stimulate cell proliferation by increasing or combined with a suitable carrier in pharmaceutical compositions, which cc associated with cell proliferation, especially cancers. Antibodies specific for PRAT may be used directly as antagonists, or indirectly as a targeting or delivery mechanism to bring pharmaceutical agents to pray expression and to monitor therapeutic interventions. The polynucleotide encoding PRAT, or complementary cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relating to polypeptide expression or monitor PRAT regulation cd diseases relation sequence sequence 933 BP; 198 A; 254 C; 236 G; 245 T;
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WO9837418-A2.
27-AUG-1998.
                                                                                                                                                                      WPI: 98-480805/41.

Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers

Claim 1; Page 42; 141pp; English.

This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate protein.
                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP. Dillon DC, Xu J; WPI; 98-480805/41.
                                                                                                                                                                                                                                                                                                                                            25-FEB-1998; U03690.
09-FEB-1998; US-904809.
25-FEB-1997; US-806596.
01-AUG-1997; US-904809.
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human; prostate cancer;
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WO9837093-A2.

27-AUG-1998.
25-FEB-1998; US-020956.
25-FEB-1998; US-020956.
25-FEB-1997; US-806099.
01-AUG-1997; US-904804.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
Polypeptides comprising immunogenic portions of prostate protesused in a vaccine for the treatment of prostate cancer Claim 3; Page 41; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic of a prostate tumour protein. The encoded immunogen, or the DNA can be used as a vaccine for the treatment of prostate cancer.

was identified by analysis of a subtracted cDNA library obtaine subtracting a prostate tumour cDNA expression library with a not tissue cDNA library.

Sequence 801 BP; 209 A; 208 C; 198 G; 164 T;
                                                                                                    Dillon DC, Xu J;
WPI; 98-609886/51.
                                                                                                                                                                                                     06-JAN-1999 (first entry)
3' cDNA sequence of prosta
Prostate; cancer; tumour;
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Homo saptens.

WO9837418-A2.
27-AUG-1998; U3690.
25-FEB-1998; US-904809.
25-FEB-1997; US-806596.
01-AUG-1997; US-904809.
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Pred. No. 1.5e
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Dillon DC, Xu J;
WPI; 98-480805/41.
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Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers
Claim 1; Page 42; 141pp; English.
This sequence represents a human prostate tumour specific gene, and car be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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Pred. No. 3.6e
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Matches 647
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WO9837093-A2.

27-AUG-1998.

25-FEB-1998; U03492.

09-FEB-1998; US-020956.

25-FEB-1997; US-806099.

01-AUG-1997; US-904804.

(CORI-) CORIXA CORP.

Dillon DC, Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 41-42; 30pp; English.
The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon
WPI; 9
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TGGAACACCACCATGAAAGGG---
                           CTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCCTCATTTGCTG
                                                                                                                                                    GTGGAGCCTCAGCAGTTCCCTCTTTCAGAACTCACTGCCAAGAGCCCTGAACAGGAGCCA 120
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                                                                CGGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTG
                                                                                                                                           GTGGAGCCTCAGCAGTTCCCTCTTTCAGAACTCACTGCCAAGAGCCCTGAACAGGAGCCA
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Pred. No. 3.6e
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 -CTCAAGTGCTGTGGCTTCACCAACTATACGG---AT
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PN W0937418-A2.

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PD 27-AUG-1998; U03690.

PF 25-FEB-1998; US-904809.

PR 25-FEB-1998; US-904809.

PR 10-AUG-1997; US-904809.

PR (1-AUG-1997; US-904809.

PR (1-AUG-1998; US-904809.

PR (1-AUG-1998); US-904809.

PR (1-AUG-198); US
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Best Local Similarity 94.9
Matches 650; Conservative
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of prostate tumour
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1 Dillon DC, Xu J;

WPI; 98-609886/51.

Polypeptides comprising immunogenic portions of prostate proteins -

Polypeptides comprising immunogenic portions of prostate proteins -

Polypeptides comprising immunogenic portions of prostate cancer

Claim 3; Page 40; 130pp; English.

Colaim 3; Page 40; 130pp; English.

Cof a prosent sequence is a new DNA which encodes an immunogenic portice

Cof a prostate tumour protein. The encoded immunogen, or the DNA itself

Cof a prostate tumour protein the treatment of prostate cancer. The DN

Companies of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal color of tissue cDNA library.

Sequence 729 BP; 157 A; 203 C; 165 G; 191 T;
                                                                                                                                                                                                                                                                                                         Query
Best L
                                                                                                                                                                                                                                                                                     Matches
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27-AUG-1998.
29-FEB-1998.
09-FEB-1998.
US-02056.
25-FEB-1997.
US-806099.
01-AUG-1997.
US-904804.
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5' cDNA sequence of prostate tumour clone N1-1862.
Prostate; cancer; tumour; vaccine; immunogen; clone;
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G-TGGAACACCACCATGAAAGGGCTCAAGTGCTGTGGCTTC-ACCAACTATACGGATTTT
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650; Conserv
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                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                Score 560.8; DB 1;
Pred. No. 3.3e-157;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                             Length
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A itself,
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RESULT 14
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ID V58489;
AC V58489;
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Query Match 41.0%; Best Local Similarity 88.0%; Matches 654; Conservative

Score 528.4; DB 1; Pred. No. 1.5e-147; 0; Mismatches 75;

Length . Indels

Gaps

9

751;

Š 밁 Š

121

741

GTGGAGCCTCAGCAGTTCCCTCTTTCAGAACTCACTGCCAAGAGCCCTGAACAGGAGCCA

180

13

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                                                                                                                                                                                                                                                                                                                                                                                                  용
                                   1 06-AN-1999 (first entry)
2 3' cDNA sequence of prostate tumour clone N1-1862.
3' prostate; cancer; tumour; vaccine; immunogen; clone; Homo sapiens.
5 Homo sapiens.
6 27-AUG-1998.
7 25-FEB-1998; US-020956.
8 09-FEB-1998; US-020956.
8 25-FEB-1997; US-806099.
9 10-AUG-1997; US-806099.
10 1-AUG-1997; US-904804.
10 CORI-) CORIAG CORP.
10 Dillon DC, Xu J;
11 Dillon DC, Xu J;
12 PR WPI; 98-609886/51.
Polypeptides comprising immunogenic portions of prostate used in a vaccine for the treatment of prostate cancer
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The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itsecan be used as a vaccine for the treatment of prostate cancer. The invariant of a subtractine by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.

Sequence 751 BP; 188 A; 196 C; 167 G; 156 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 41.0%; al Similarity 88.0%; 654; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 528.4;
; Pred. No. 1.5e
0; Mismatches
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1.5e-147;
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GenCore version 4.5 Copyright (c) 1993 - 1998 Comp

Compugen Ltd.

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Title:

US-09-030-606-111 1289 1 AGCCAGGCGTCCCTC

Database Searched: Scoring table: Sequence: Perfect score:

Issued_Patents_NA:*

176461 seqs, 45838279 residues

IDENTITY_NUC

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/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*

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September 25, 1999, 07:29:01; Search time 165.01 Seconds (without alignments) 716.145 Million cell updates/sec
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APPLICANT: Hilm.... Olga
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.

APPLICANT: Goli, Surya K.

APPLICANT: Guegler, Karl J.

APPLICANT: Guegler, Karl J.

ITILE OF INVENTION. NEW TRANSMEMBRANE PRO
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, In
STREET: 3174 Porter Drive
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                                                                                                                                                                                              ; IMMEDIATE SOURCE:
; LIBRARY: MYOMNOTO1
; CLONE: 779308
US-08-855-140-2
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US-08-855-140-2
                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                               Query Match
Best Local Similarity
Matches 248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,140
FILING DATE: Herewith
CLASSIFICATION: 435
CRISTIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                               181 TGTGTGGTGCAGCCCTGTTGGCCAGTGGGCCATCTGGGTGTCAATCGATGGGGCCATCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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PCT-US95-09941-1

US-08-118-101A-1

US-08-469-412A-6

US-08-469-412A-6

US-08-148-215A-1

US-08-299-849B-24

US-08-299-849B-25
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                                                                                                                              Score 83.4; DB 4; Pred. No. 6.1e-16;
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9CT-US91-04986-1
US-08-254-493-3
US-08-254-493-3
US-08-254-493-3
US-08-258-463-1
US-08-408-2228-3
US-08-63-631-200-11
US-08-631-200-11
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Patent No. 5863735
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer L.
APPLICANT: GO11, SUTYA K.
TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
NUMBER OF SEQUENCES: 4
                                                         IMMEDIATE SOURCE:
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CITY: Palo Alto
STATE: CA
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                                                                                                                nucleic acid
                    663655
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                                        SCORNOT 01
                                                                             linear
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Best Local Sim
Matches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08807044 Patent No. 5863735
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDION TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRATESC for Windows Version 2.
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/807,044
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNMER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429
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                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
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CITY: Palo Alto
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Local Similarity 55.9%;
    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGCTGTGGTCGCCTTGGTGTACACCACAATGGCTGA 466
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                     nucleic acid
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                                       1452 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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single
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                                                                                                                                                                                    PF-0224 US
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; LIBRARY: GenBank
; CLONE: 180140
US-08-807-044-4
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PCT-US91-04986-1
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GENERAL INFORMATION:
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Best Local Similarity
Matches 173; Conserv
                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/04986
FILING DATE: 19910715
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
TITLE OF INV
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/553,759
FILING DATE: 13-JUL-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Rapid Immunoselection Cloning Method NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                             COUNTRY:
APPLICATION NUMBER: US 07/498,809 FILING DATE: 23-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                Colorado
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                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simmons, David L.
Stamenkovic, Ivan
Stengelin, Siegfried
                                                                                                                                                                                                                                                                                                                                                                                                                                               Amiot, Martine
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Camerini, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lauffer, Leander
Oquendo, Carmen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seed, Brian
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51.2%;
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Pred. No. 1.4e-09;
D; Mismatches 162;
                                                                                                                                                                                     Version
                                                                                                                                                                                     #1.25
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RESULT 5
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PCT-US91-04986-1
                                                                                                                                                                                                                                         Sequence 2, Application Patent No. 5439886
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.9%;
Best Local Similarity 51.2%;
Matches 173; Conservative
                                                                                                        APPLICANT: IKEYAMA, SHUICHI
APPLICANT: KOYAMA, MASARU
APPLICANT: MIYAKE, MASAYUKI
APPLICANT: SENOO, MASAHARU
TITLE OF INVENTION: MONOCLONAL AN
TITLE OF INVENTION: PRODUCTION THUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 13-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 25-FEB-198
ATTORNEY/AGENT INFORMATION:
NAME: Wall, Margaret M.
REGISTRATION NUMBER: 33.46
REFERENCE/DOCKET NUMBER: 1
                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 303-499-8080
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                                                                                                                                                                                                                                                                                                                                                                                      493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 ACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 AGTGCTCTTCCATAACCTCCCCTCCCTCACGCTGGGCAATGTGTTTGTCATCGTGGGCTC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1452 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear
                STATE: MASSACHUSETTS
                                    CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                    ATTTCTGCAGTGTTGTGGTATAATGGCACGAGTGATT 530
                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCAAGAAAGATTATGGTTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACCATGAA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGCTCTTTGTATATGAACAGAAGCTGAATGAGTATGTGGC---TAAGGGTCTGACCGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCGCCTTGGTGTACACCACAATGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTATGTCGTTCATCCTGCTGCTGATTATCCTCCTTGCTGAGGTGACCTTGGCCAT
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Pred. No. 1.4e-09;
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                                                                        DIKE, BRONSTEIN, ROBERTS & CUSHMAN
                                                                                                                              ANTIBODY,
                                                                                                                                                    POLYPEPTIDES AND
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REFERENCE/DOCKET NUMBER: 41777
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-3400
TELEFAX: (617) 523-6440
TELEFAX: (617) 523-6440
TELEFAX: 6010 NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 149; Conserv
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HYPOTHETICAL: N
ANTI-SENSE: NO
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APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 08 FILING DATE: 17-APR-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
ADDITARTION NUMBER: TO COSTOCE TO COST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 GCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTTTCTGTGTGGTG 189
317 CGGC_320
                                           430 CTGC 433
                                                                                     257
                                                                                                                                                                       197
                                                                                                                                                                                           310 CCGGCGTTGTGGTCTTTGCTCTTGGGTTTCCTGGGCTATGGTGCTAAGACTGAGAGCA 369
                                                                                                                                                                                                                                                    137 AGCAAGAAACTAATAATAATTACCAGCTTCTACACAGGAGTCTATATTCTGATCGGAG 196
                                                                                                                                                                                                                                                                                                                                                                              190 CAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATGGGGCATCCTTTCTGAAGATCT 249
                                                                                                                          370 AGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCATCTTCATTGCTGAGGTTGCAG 429
                                                                                                                                                                                                                                                                                               250 TCGGGCCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL TYPE: BREAST CARCINOMA CELL LINE: ZR-75-1
                                                                                                                                                                                                                                                                                                                                       77 TIGCTGTCCTTGCCATTGGACTATGGCTCCGATTCGACTCTCAGACCAAGAGCATCTTCG 136
                                                                                                                                                                                                                                                                                                                                                                                                                          17 GCACCAAGTGCATCAAATACCTGCTGTTCGGATTTAACTTCATCTTCTGGCTTGCCGGGA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 022321-1992 FILING DATE: 07-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                   CCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGGCTGTGCAGGAGTCCC
                                                                                AGTGCATGCTGGGACTGTTCTTCGGCTTCCTCTTGGTGATATTCGCCATTGAAATAGCTG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESNICK, DAVID S
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Pred. No. 1.1e-07;
0; Mismatches 155
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RESULT 6
US-08-254-493-3
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US-08-254-493-3
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/865552
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION NUMBER: JP 085396-1991
FILING DATE: 17-APR-1991
FILING DATE: 17-APR-1991
                                                                      FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 022321-1992
FILING DATE: 07-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,493
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONL
STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-FEB-1992 ATTORNEY/AGENT INFORMATION:
                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND TITLE OF INVENTION: PRODUCTION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                ORIGINAL SOURCE:
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                                                                                                                                                                                               ANTI-SENSE: 1
                                                                                                                                                                                                                               OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: RESNICK, DAVID S. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U:
ZIP: 02109
                                                                                                                         CELL TYPE:
                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: BOSTON
                                      NAME/KEY:
                                                                                                                                                            ORGANISM:
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MIYAKE, MASAYUKI
SENOO, MASAHARU
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                                                                                                                                            BREAST CARCINOMA
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Query Match

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Score 56;

DB 1;

Length 1120;

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RESULT 7
US-08-408-222B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ikeyam
APPLICANT: Koyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Koyama, Masaru
APPLICANT: Miyake, Masauyki
APPLICANT: Senoo, Masaharu
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/2: FILING DATE: 06-JUN-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                      APPLICATION NUMBER: JP-022321-1992
FILING DATE: 07-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-085396-1991
FILING DATE: 14-APR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130 W
                                       REFERENCE/DOCKET NUMBER: 41777-DIV
                                                      NAME: Resnick, David S. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                   APPLICATION NUMBER: JP-0'
FILING DATE: 12-APR-1991
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 22-MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACCAAGTGCATCAAATACCTGCTGTTCGGATTTAACTTCATCTTCTGGCTTGCCGGGA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGC 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGGGCCACTGTCCAGTGCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTTTCTGTGTGGTG 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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0; Mismatches 155;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
TRUGTH: 687 base pairs
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ikeyama,
APPLICANT: Koyama,
APPLICANT: Miyake,
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08408222B Patent No. 5776727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 149; Conserv
                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: hum
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                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES NUMBER OF SEQUENCES: 7
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STATE:
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   FILING DATE:
                                                                                      COMPUTER: IBM Compatible
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                  APPLICATION NUMBER:
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Miyake, Masauyki
Senoo, Masaharu
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Pred. No.
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RESULT 9
US-08-332-463-14
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ANTI-SENSE:
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LENGTH: 1120 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER:
FILING DATE: 14-APR-
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APPLICATION NUMBER: JP-079996-1991
FILING DATE: 12-APR-1991
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LOCATION: 112...79
OTHER INFORMATION:
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les 149; Conserv
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                                                                                                 CGGC 431
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Pred. No. 1.4e-07;
0; Mismatches 155
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Best Local S
Matches 26
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APPLICANT: DORNER, F.
APPLICANT: SCHEITLINGER, F.
APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC-COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                  IMMEDIATE SOURCE:
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                                                                                                                                                                                                           146 GACCATGATGATCCTCTTCAATTTGCTCATCTTTCTGTGTGGTGCAGCCCTGTTGGCAGT 205
326 TGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCCTCGTGAC 385
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ZIP: 22313-0299
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STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                   CAGTGCCATGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTT 325
                                                                                                       GGGCATCTGGGTGTCAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCCACTGTCGTC 265
                                                                                                                                                                          121.
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US-08-060-822A-4
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US-07-603-451A-4
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Best Local Similarity
Matches 85; Conserv
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Patent No. 5202420
           Sequence 4, Application Patent No. 5432270
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
                                                                                                                            1188 ATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAGGCACTTCA 1247
                                                                                                                                                                                                                                                                       1128 TGCCCCCTAGGCCTAGTGGTGATCCCAGTGCTCTACTGGGGGATGAGAGAAAGGCATTTT 1187
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LENGTH: 349 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bevins, Charles
APPLICANT: Diamond, Gill
APPLICANT: Zasloff, Michael
                                                                                                              304
                                                                                                                                                                             244
                                                                                                                                                                                                                                         386 GTTCTTCTTCATCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCCTT 445
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Patricia A. Schreck
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: CH-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: UPPLICATION NUMBER: UPPLICATION: 19901025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 19103
                                                                                                            ACAGCCGGGATCAATGCCCAGTCAGAAACTGCGCCCTTTGACAGAGCGTCTAAAATTTAA 303
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                                                                                                                                                                                                                                                                                                           Conservative
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                              US/08060822A
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                                                                                                                                                                                                                                                                                                        Score 38.8; DB 1; Length 349; Pred. No. 0.012; O; Mismatches 77; Indels
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PCT-US94-05257-4
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APPLICATION NUMBER: US/08/060,822/
FILING DATE: 19930511
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,200
APPLICATION NUMBER: 07/991,200
                                                                                                                                                                                                                                  Sequence 4, Application PC/TUS9405257 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock
                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Rebecca Ralph Gaumond REGISTRATION NUMBER: 35,152 REGISTRATION NUMBER: CHARLECOMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                                      APPLICANT: Bevins, Charles L. APPLICANT: Diamond, Gill APPLICANT: Zasloff, Michael
                                                                                                                                                                                                                                                                                                                                                                                              1128 TGCCCCCTAGGCCTAGTGGTGATCCCAGTGCTCTACTGGGGGATGAGAGAAAAGGCATTTT 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 349 base pairs
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bevins, Charles L.
APPLICANT: Diamond, Gill
APPLICANT: Zasloff, Michael
TITLE OF INVENTION: No. 5432270el Antimicrobial Peptides
                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1188 ATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAGGCACTTCA 1247
                                                                                                                                                       TITLE OF INVENTION: Novel Antimicrobial Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucle4c acid
STRANDEDNESS: double
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                                   CITY: Philadelphia
STATE: Pennsylvania
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                COUNTRY:
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Similarity 52.5%;
85; Conservative
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19103
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REFERENCE/DOCKET NUMBER: CH-0408
FELECOMMUNICATION INFORMATION:
FELEPHONE: (215) 568-3100
FELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERIT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                             tent No. 5618720
                                                                                                                                                                                                     APPLICANT: Schwartz, Arnold
APPLICANT: Brenner, Robert
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
NAITHIN, Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1128 TGCCCCCTAGGCCTAGTGGTGATCCCCAGTGCTCTACTGGGGGGATGAGAGAAAGGCATTTT 1187
CURRENT APPLICATION DATA: - APPLICATION NUMBER: US
                                                                                 COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1188 ATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAGGCACTTCA 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/060,822
FILING DATE: May 11, 193
APPLICATION NUMBER: 07/991,200
FILING DATE: December 15, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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SOFTWARE: WORDPE
                                                                                                                                                            CITY: San Diego
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucle4c acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Rebecca Ralph Gaumond REGISTRATION NUMBER: 35,152
                                   SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                               ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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FILING DATE: 11-MAY-1994
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                                                                                                                                                                                                                                                                                                             Williams, Mark E.
Harpold, Michael Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 base pairs
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                                                     IBM Compatible
SYSTEM: DOS
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US/08/404,354B
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; NAME/KEY: Coding Sequence
; LOCATION: 79...5700
; OTHER INFORMATION:
US-08-404-354B-1
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US-08-314-083B-1
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Applic Patent No. 5686241
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Best Local :
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                                                                                                                                                                                                                             APPLICANT: Ellis, Steven Bradley APPLICANT: Williams, Mark E. APPLICANT: Harpold, Michael Miller APPLICANT: Schwartz, Arnold APPLICANT: Brenner, Robert TITLE OF INVENTION: CALCIUM CHANNEL NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-FEB-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 28-SEP-19
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
OPERATING SYSTEM: DOS
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REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
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                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 GCTTCCTGTTCCACCAGGACGCCTACCTGCGCAGCGGCTGGAACGTGCTGGACTTCATCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8%;
Local Similarity 53.1%;
nes 77; Conservation
                                                                                                       COUNTRY: USA
ZIP: 92101-2926
                                                                                                                                             STATE:
                                                                                                                                                            CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-238-0062
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                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5975 base pairs
TYPE: nucleic acid
                SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                             CA
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                                                                                                                                                                                                                                     Brenner, Robert
VENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
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                                   IBM Compatible
SYSTEM: DOS
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Pred. No. 0.4;
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APPLICATION NUMBER: FILING DATE: 28-SE

JMBER: US/08/314,083B 28-SEPT-1994

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                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08435675B
Patent No. 5710250
GENERAL INFORMATION:
APPLICANT: Ellis, Steven Bradley
APPLICANT: Williams, Mark E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.8%;
Best Local Similarity 53.1%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53191
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 5975 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sinc'
TOPOLOGY
                                                                                                                                                                                                                                                                                                         APPLICANT:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                       ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                           APPLICANT: Brenner, Robert
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 TCGTCTTCCTGGGGGTCTTCACGGC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 GCTTCCTGTTCCACCAGGACGCCTACCTGCGCAGCGGCTGGAACGTGCTGGACTTCATCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 GTTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCCTCGTGACGTTCTTCT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 TGGAGTACTTCTTCCTCACCGTCTTCTCCATCGAAGCCGCCATGAAGATCATCGCCTACG 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence LOCATION: 79...5700
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                       STREET: 1660 Uni
                                                                                                                                 COUNTRY:
                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                         1660 Union Street
                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                       Harpold, Michael Miller
Schwartz, Arnold
                                                     IBM Compatible
                                                                                                                                                                                                               Brown, Martin, Haller & McClain
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Search completed: September 25, 1999, 07:29:04 Job time: 3381 sec

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Best Local Similarity 53.1%;
Matches 77; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 619-238-0999
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                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
464 TCGTCTTCCTGGGGGTCTTCACGGC 488
                                                                    404
                                                                                                                                        274 TGCAGTTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTG 333
                                 394 TCATCCTCCTCCTCATCTTCATTGC 418
                                                                                                   334 GITTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 013 -0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53193
                                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 79...5700
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                    GCTTCCTGTTCCACCAGGACGCCTACCTGCGCAGCGGCTGGAACGTGCTGGACTTCATCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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Pred. No. 0.4;
0; Mismatches
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Title:
Perfect score:
Sequence:
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/cgn2_6/ptodata/2/pna/US07_COMB.seq:*
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(without alignments)
1401.618 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query Match Length

DB ID

Description

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uence 12, uence 12,	equence 74,	13,	13,13,		17,	Sequence 16, App Sequence 16, App Sequence 16, App Sequence 16, App Sequence 16, App	1,000,000	5033, 1, Ap 82, Ap 50, Ap	Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 14, App1

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STREET: 6300 Columbia Center, 701 Fifth Avent CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,747
FILING DATE: 09-FEB-1998
CLASSIFICATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C2
REFERENCE/DOCKET NUMBER: 210121.428C2
REFERENCE/DOCKET NUMBER: 210121.428C2
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C2
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REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C2
REFERENCE/DOCKET NUMBER: 210121.428C2
REFERENCE/DOCKET NUMBER: 31,392
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REFERENCE/DOCKET NUMBER: 210121.428C2
REFERENCE/DOCKET NUMBER: 31,392
REF
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US-09-020-747-111
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Best Local Similarity
Matches 1289; Conserv
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GENERAL INFORMATION:
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APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
             301
                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                               1 AGCCAGGCGTCCCTCTGCCTGCCCACTCAGTGGCAACACCCCGGGAGCTGTTTTGTCCTTT 60
TCATCGCAGCCGGCGTTGTGCTTTGCTTTGGTTTCCTGGGCTGCTATGGTGCTAAGA
                                                                                                                                                                                                                                                                                                             CCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTTGCTCATCTTTC 180
                                               TCATCGCAGCCGGCGTTGTGGTCTTGCTCTTGGTTTCCTGGGCTGCTATGGTGCTAAGA 360
                                                                                  TGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTGGGCTACTTCC
                                                                                                          TGAAGATCTTCGGGCCACTGTCGTCCTCCAGTGCCAGTTTGTCAACGTGGGCTACTTCC
                                                                                                                                                             TGTGTGGTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTCAATCGATGGGGCATCCTTTC
                                                                                                                                                                                                                                          CCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTGCTCATCTTTC
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Pred. No. 0;
0; Mismatches
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                                                           Sequence 111, Application GENERAL INFORMATION:
         APPLICANT: Xu, Jiangchun APPLICANT: Dillin, Davin C. TITLE OF INVENTION: COMPOUNDS
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Best Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0, ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILLING DATE: 09-FEB-1998
CLASSIFICATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 7
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 base pairs
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NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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MOLECULE TYPE:
ORIGINAL SOURCE:
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STRANDEDNESS: single
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RESULT 3
US-09-030-606-111
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 7
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARRCTERISTICS:
LENGTH: 1299 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECHE TYPE: CDNA
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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
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                          ACTCACCCTACTTCAAAGAGAACAGTGCCTTTCCCCCATTCTGTTGCAATGACAACGTCA
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                                                                                                                                                                                                                                                                                                              Sequence 111, Application US/09030607 GENERAL INFORMATION:
                                 ADDRESSEE: SEED and BERRY LLP
ADDRESSEE: 6300 Columbia Center, 701 F
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
APPLICATION UMBER: US/09/030,607
FILING DATE: 25-FEB-198
CCLASSIFICATION:
                                                                                                                                                                                                                                         APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,
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; ORIGINAL SOURCE:
; ORGANISM: Homo
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDEDNESS: aingle
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1289; Conservative 0,
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CTGGAATTGGGGGCCTCGAGCTGGCTGCCATGATTGTGTCCATGTATCTGTACTGCAATC
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                                                      CCAACACAGCCAATGAAACCTGCACCAAGCAAAAGGCTCACGACCAAAAAGTAGAGGGTT
                                                                                           ACTCACCCTACTTCAAAGAGAACAGTGCCTTTCCCCCCATTCTGTTGCAATGACAACGTCA
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Pred. No. 0;
0; Mismatches
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GENERAL INFORMATION:

APPLICANT: Milcham, Davin C.

APPLICANT: Milcham, Jennifer Lynn

APPLICANT: Milcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C7

CURRENT APPLICATION NUMBER: US/09/288,946

CURRENT APPLICATION NUMBER: US/09/288,946

CURRENT FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 381

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 111

LENGTH: 1289
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GENERAL INFORMATION:
APPLICANT: Rosen et
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NT EILING DATE: 1998-09-04
ER APPLICATION NUMBER: PCT/US98/044!
ER FILING DATE: 1998-03-06
ER APPLICATION NUMBER: 60/040,162
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ER FILING DATE: 1997-03-07
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ER FILING DATE: 1997-03-07
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ER APPLICATION NUMBER: 60/040,336
ER APPLICATION NUMBER: 60/040,163
ER FILING DATE: 1997-03-07
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ER FILING DATE: 1997-05-23
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ER APPLICATION NUMBER: 60,047,613
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ER APPLICATION NUMBER: 60/043,674
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,669
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,312
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,313
ER FILING DATE: 1997-04-11

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ER APPLICATION NUMBER: 60/043,569
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,311
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,671
ER FILING DATE: 1997-04-11

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APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11

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60/047,601

NUMBER: 60 1997-05-23

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LIER FILING DATE: 1997-09-05

EARLIER APPLICATION NUMBER: 60/05

EARLIER FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 280

SOFTWARE: PATENTIN VET. 2.0

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R FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/
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ER APPLICATION NUMBER: 60/047,593
ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-04-11
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/047,501
ER FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/057
R FILING DATE: 05-Sep-1997
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ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,672
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,315
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ER APPLICATION NUMBER: 60/048,974
ER FILING DATE: 1997-06-06
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,889
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ER APPLICATION NUMBER: 60/056,899
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TITLE OF INVENTION: NOVEL CONTIGS OBTAIN
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 2041-752CON1
CURRENT APPLICATION NUMBER: US/09/359,92
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: US 09/205,15
EARLIER FILING DATE: 1998-12-03
NUMBER: OF SEO ID NOS: 13203
SOFTWARE: FASTSEQ for Windows Version 3.
SEQ ID NO 5033
SEQ ID NO 5033
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US-09-359-922-5033/c
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Best Local Similarity
Matches 1288; Conserv
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GTGGAGCCTCAGCAGTTCCCTCTTTCAGAACTCACTGCCAAGAGCCCCTGAACAGGAGCCA 120
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                                       TGCTGGTAGTGCCTGCCATCAAGAAAGATTATGGTTCCCAGGAAGACTTCACTCAAGTGT
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Pred. No. 0;
0; Mismatches
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Version #1.30

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RESULT 8
US-08-957-182-1
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                                                                                            APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racle, Lisa A.
APPLICANT: Racle, Lisa A.
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael
TITLE OF INVENTION: SECRETED PF
TITLE OF INVENTION: TRECODING TH
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1020
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                       ADDRESSEE: Genet.
STREET: 87 Cambr
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
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                                                                        E: Genetics Institute,
87 CambridgePark Drive
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McCoy, John M.
LaVallie, Edward R.
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; STRANDENNES: double
; TOPOLOGY: linear
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NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1605 base pairs
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Best Local Similarity
Matches 1287; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           421
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                                   ACTCACCCTACTTCAAAGAGAACAGTGCCTTTCCCCCATTCTGTTGCAATGACAACGTCA
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Pred. No. 0;
0; Mismatches
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US-09-148-545-82 Sequence 82, Application US/09148545 GENERAL INFORMATION: APPLICANT: ROSen et al. TITLE OF INVENTION: 70 Human Secreted Proteins FILE REFERENCE: PZ001P1 CURRENT APPLICATION NUMBER: US/09/148,545 CURRENT FILING DATE: 1998-09-04 EARLIER FILING DATE: 1998-09-06 EARLIER FILING DATE: 1997-03-07 EARLIER APPLICATION NUMBER: 60/040,162 EARLIER APPLICATION NUMBER: 60/040,33 EARLIER APPLICATION NUMBER: 60/040,33 EARLIER APPLICATION NUMBER: 60/038,621 EARLIER FILING DATE: 1997-03-07 EARLIER APPLICATION NUMBER: 60/040,161 EARLIER FILING DATE: 1997-03-07 EARLIER APPLICATION NUMBER: 60/040,626 EARLIER APPLICATION NUMBER: 60/040,334 EARLIER APPLICATION NUMBER: 60/040,334 EARLIER APPLICATION NUMBER: 60/040,336 EARLIER FILING DATE: 1997-03-07 EARLIER APPLICATION NUMBER: 60/040,336 EARLIER FILING DATE: 1997-03-07 EARLIER APPLICATION NUMBER: 60/040,336 EARLIER FILING DATE: 1997-03-07 EARLIER FILING DATE: 1997-03-07 EARLIER APPLICATION NUMBER: 60/040,336 EARLIER FILING DATE: 1997-03-07 EARLIER FILING DATE: 1997-03-07	Qy 1140 CTAGTGGTGATCCCAGTGCTCTACTGGGGATGAGAGAGAG	1215 ACCUTGCCAAGCAGCAGTGATTGGGGGAAGGAACGAACCTACAATGTCACCTTGGGCCA 961 GAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGCTAGATAGGGACCACTCCTTTTA-GC	975 CCAACAGCCAATGAAACCTGCACCAAGCAAAAAGGCTCACGACCAAAAAGTAGAGGGTT 103 721 GCTTCAATCAGCTTTTGTATGACATCCGAACTAATGCAGTCACCGTGGGTGG
EARLIER APPLICATION NUMBER: 60/043,580 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,568 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,314 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,311 EARLIER APPLICATION NUMBER: 60/043,671 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,674 EARLIER APPLICATION NUMBER: 60/043,312 EARLIER APPLICATION NUMBER: 60/043,312 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,312 EARLIER APPLICATION NUMBER: 60/043,315 EARLIER APPLICATION NUMBER: 60/043,315 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-06-06 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,877 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22	FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047.5 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047.5 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047.6	A FILING DATE: 1997-0 A APPLICATION NUMBER: FILING DATE: 1997-0 A APPLICATION NUMBER: FILING DATE: 1997-0 A PPLICATION NUMBER:	ING DATE: 1997-05-2 LICATION NUMBER: 60

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ER APPLICATION NUMBER: 60/056,631

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,845

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ER APPLICATION NUMBER: 60/056,892

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                                                       ER APPLICATION NUMBER: 60/043,578
ER FILING DATE: 1997-04-11
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Sequence 4, Application US/09010146
GENERAL INFORMATION:
APPLICANT: N1, et al.
TITLE OF INVENTION: Polynucleotid
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: U:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: W
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
'COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                   CURRENT APPLICATION DATA:
                                                                                                             ADDRESSEE: Human Genome Sci
STREET: 9410 Key West Ave
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
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; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (ger
US-09-010-146-4
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ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF354PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPHONE: 301-309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1288 base pairs
TYPE: nucleic acid
GTEANDENNESS: signing
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Best Local Similarity 99.8%;
Matches 1284; Conservative
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                                                                                CCCTACTTCAAAGAGAACAGTGCCTTTCCCCCATTCTGTTGCAATGACAACGTCACCAAC
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0; Mismatches
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RESULT 11
US-09-010-146-50/c
Sequence 50, Application US/09010146
GENERAL INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US98/00959
FILING DATE: 21-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF354PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPHONE: 301-309-8504
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TELEPHONE: 301-309-8504
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                            APPLICANT: N1, et al.
TITLE OF INVENTION: Polynucleotides and
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Invention of the second sciences of the second sciences
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomi
US-09-010-146-50
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Best Local Similarity
Matches 1284; Conserv
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RESULT 12
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 933 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT26
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08808148
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
APPLICANT: Goli, Surya
APPLICANT: Zhang, Hong Wolfe
TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0218 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                      APPLICATION NUMBER: US, FILING DATE: Herewith CLASSIFICATION: 514
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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STATE: CA
COUNTRY: USA
ZIP: 94304
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3174 Porter Drive
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Matches
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Local Similarity 100.0%;
Les 928; Conservative
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
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Best Local Similarity 98.9%;
Matches 624; Conservative
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 49
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                                395 CATCCTCCTCCATCTTCATTGCTGAGGTTGCAGCTGCTGTTGGTCGCCCTTGGTGTACAC 454
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STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/740,274
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TTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTT 394
                                                                                                                                                                                                                                                                                           GTGTCAATC-GATGGGGCATCCTTTCTGAAGATCTTCGGGGCCACTGTCGTCCAGTGCCAT
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                                                                                                                                    TTTCCTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGNGACGTTCTTCTT
                                                                  CATCCTCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACAC
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Lavallie, Edward
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Pred. No. 9e-175;
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; TYPE: nucleic acid; STRANDEDNESS: sing; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-806-099-16
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                                                                                                                             Query Match
Best Local Sim
Matches 714;
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/806,099
FILING DATE: 24-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.427
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-667-5728
TELEPAX: 206-667-5728
                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-667-5728
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 801 base pairs
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ADDRESSEE: Janet Sle
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STATE: V
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Pred. No. 1.7e-171;
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GENERAL INFORMATION:
APPLICANT: Xu. Jiangchun
TITLE OF INVENTION: COMPOUNDS FO
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION GRAPHICATION DATA:
APPLICATION UNMBER: US/08/806,596
FILING DATE: 24-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428
                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                         STREET: 1124 COCITY: Seattle
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
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Best Local Similarity 91.7%;
Matches 714; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 801 base pairs
TYPE: nucleic acid
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94764162	A1660579	IMAGE:2346245 3' similar to TR:060635 060635 TSPAN-1. [1] ;, mRNA	we68d03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone	AI660579 697 bp mRNA EST 10-MAY-1999		

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TGGGAACTGTGAAGAGGCACCCTGGCAAGCAGCAGTGATTGGGGGGAGGGGACAGGATCTA 942
                                                                                          TGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCTGCCACTACTGCCGCCACA 882
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                                     TGTATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCTGCCACTACTGCCACA
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Email: Robert 7
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 697)
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/db_xref="taxon:9606"
/map="between D11S1765 and UGB"
/clone="IMAGE:2346245"
/clone=11b="Soares_Dieckgraefe_colon_NHCD"
/tlssue_type="colonic mucosa from 3 patient
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g1647216
AA100799.1
                                                     This clone is available royalty-free through LLNL:
IMAGE Consortium (info@image.llni.gov) for further
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 353.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 593)

Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Chissoe, S., Dietrich, N., Kucaba, T., Lecy, M., Le, N., Le, N.,

Hawklins, M., Moore, B., Morris, M., Parsons, J., Prange, C., Rikhin, L.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikhin, L.,

Mardis, E., Moore, B., Morris, M., Soares, M.B., Tan, F., Thierry-Meg, J.,
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IMAGE:526753 3', mRNA sequence.
                                                                                                                                                                     Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should k
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                Generation and analysis of 280,000 human Genome Res. 6 (9), 807-828 (1996) 97044478
On May 8, 1995 this sequence version repl
                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
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/organism="Homo sapiens"
/db_xref="GDB:3918182"
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                            Komo sapiens
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Pred. No. 1.1e-141;
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                 CTAAGGTAGCCAGTCTGTTGCCCCATTCCCCCAGTCTATTAAACCCTTGATATGCCCCCCT
                                            GCCAGAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGGCTAGATAGGGACCACTCCTTTT
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546;
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Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult, age 25"
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/sex="male"
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/db_xref="taxon:9606"
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Pred. No. 3.7e-134;
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1 (bases 1 to 562)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189085.
                                                                                                                                                                                                                                                                                                                     Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI720370 562 bp mRNA EST 10-JUN-1999 as75g12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334598 3' similar to TR:060635 060635 TSPAN-1. [1] ;,
                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available roya
                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Fax: 314 286 1810
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                                                                                              /clone_lib="Barstead colon
/sex="male"
                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2334598"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro Tumor Gene Index Unpublished (1997)
On May 5, 1995 this sequence version replaced gi:798
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AA659332.1
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Tel: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA659332 607 bp mRNA EST 03-DEC-1997 nul3d10.sl NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1207891, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                       AATGTCACTTGGGCCAGAATGGACCTGCCCTTTCTGCTCCAGACTTGGGGCTAGATAGGG
                                                       TTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAGGCACT 1244
                                                                                                               TTCCAGAGCCTCTAAGGTAGCCAGTTCTGTTGCCCCATTCCCCCCAGTCTATTAAACCCTTG
                                                                                                                                                                                                                TATCTGTACTGCAATCTACAATAAGTCCACTTCTGCCTCTGCCACTACTGCTGCCACATG
                                         TTTATAGCCT-GGCATAAGTG-AATCAGCAGAG-CTCTGGGTGGATGTGTAGAAG--CAC
                                                                                                ATATGCCCCCTAGGCCTAGTGGTGAT-CCAGTGCTCTACTGGGGGATGAGAGAAA-GCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq primer: -40ml3 fwd. ET from High quality sequence stop: 429. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 739
152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pAMP10; Site_1: Not1; Site_2: EcoR1; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoR1 adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1207891"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 478.2; DB 36; Length 607; Pred. No. 4.9e-123;
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                                                                      479
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                                                                   CCTCGAGCTGGCTGCCATGATTGTGTCCATGTATCTGTACTGCAATCTACAATAAGTCCA 420
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consorttum/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1404881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 479)
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                /note-"Vector: pamp10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of FCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pamp10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:745907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="45 years old"
/lab_host="DH10B"
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99.8%;
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                                                                                                                                                                                   Score 477.4; DB 33; Pred. No. 7.4e-123;
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                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D
DNA Sequencing by: Washington University Genome Sequencing Cen
Clone distribution: NCI-CGAP clone distribution information ca
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
On Sep 12, 1996 th
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nc78e09.rl NCI_CGAP_Pr2
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                       primer:
                                                                                                                                                                                                                                                                           -bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                 rt Length: 703 Std Error: 0.00
primer: -28m13 rev1 ET from Amersham
quality sequence stop: 442.
Location/Qualifiers
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                                                                         /clone_lib="NCI_CGAP_Pr2"
/sex="Male"
                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:783496"
/note="Vector: pamPl0; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
                                   /dev_stage="45 years old"
/lab_host="DH10B"
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Homo
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AA593864.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                        AA593864 470 bp mRNA EST 25-SEP-1997 an19408.sl NCI_CGAP_Col2 Homo sapiens cDNA clone IMAGE:1084359 3',
                                                                                 Homo sapiens
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AA593864
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                                                                  Vertebrata;
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Tumor Gene Index

Project (CGAP),

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                                                                                         CTGGGGGATGAGAGAAAGGCATTTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Procurement: L. Jeffrey Medeiros, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1084359"
/clone_lib="NCI_CGAP_Co12"
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488 GGGCCTNCGAGCTGCCATGATTGTGTCCATGTATCTGTACTGCCAATCTACAATAA 429
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1834 Std Error: 0.00
Seq primer: -40413 fwd. from Amersham
High quality sequence stop: 434.
Location/Qualifiers
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Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Mardis,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="bHJ08 (ampicillin resistant)
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/dev_stage="19 weeks"
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/clone="IMAGE:376003"
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/db_xref="GDB:1284259"
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                                                                                                                                                                                                      35.4%;
99.0%;
                                                                                                                                                                                                      Score 456.8; DB 27; Pred. No. 4.2e-117;
                                                                                                                                                                    Mismatches
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849 GTCCACTTCTGCCTCTGCCACTACTGCCACATGGGAACTGTGAAGAGGCACCCTGGC 908

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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 th
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AA846269
                                                                                                        High
                                                                                                                     Insert Length: 1547
Seq primer: -40ml3 f
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1 (bases 1 to 446)
                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                         cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can by
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                              www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                 Bonaldo, Ph.D.
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                                                                                          primer: -40ml3 fwd. ET from Amersham
quality sequence stop: 437.
   Location/Qualifiers
                                                                                                                                                                                                                                                                       (301) 496-1550
/organism-"Homo sapiens"
/db_xref="taxon:9606"
/map-"672C09; 17; 17p11.2; 21q"
/clone-"IMAGE:1387451"
/clone_11b-"Soares_parathyroid_tumor_NbHPA"
/tissue_type-"parathyroid tumor"
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                                                                                                                                   Std Error:
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836 CAATCTACAATAAGTCCACTTCTGCCTCTGCCACTACTGCTGCCACATGGGAACTGTGAA 895
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Eukaryota; Metazoa; Ceutheria; Primates; Ceutheria; Primates; Ceutheria; Primates; Ceutheria; Ceuth
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AI075023.1
                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pT7T3D
/note="Organ: parathyroid gland; Vector: Site_1:
Site_2: Eco RI; lst strand cDNA was primed with
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pred. No. 1.2e-113;
0; Mismatches 1;
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                                                                                                                                                                      ATTTTATAGCCTGGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTAGAAGGCA 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATTCCAGAGCCTCTAAGGTAGCCAGTTCTGTTGCCCCATTCCCCCAGTCTATTAAACCCT 1122
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Seq primer: -40ml3 fwd.
High quality sequence st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity 99.8%;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="colon tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="organ: colon; Vector: Bluescript SK-; Site_1:
/note="organ: colon; Vector: Bluescript SK-; Site_1:
/note="organ: colon; Cloned unidirectionally. Primer:
/noted colon tumors. 5' adaptor sequence: 5'
/noted colon tumors. 5' adaptor sequence: 5'
/noted colon tumors. 5'
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/db_xref="taxon:9606"
/clone="IMAGE:1594333"
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/sex="mixed"
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wd. ET from Amersham
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GACATCCGAACTAATGCAGTCACCGTGGGTGGTGGTGGCAGCTGGAATTGGGGGCCCTCGAG
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AA659579
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cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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1 (bases 1 to 453)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
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High quality sequence stop: 436.
Location/Qualifiers
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Unpublished (1997)
On May 8, 1995 this sequence version replaced g1:801529
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//lab_host="DHIOB"
//lab_host="DH
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/db_xref="taxon:9606"
/clone="IMAGE:1203155"
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                                                                                                                                                                                                                                                                                                                                       33.9%;
                                                                                                                                                                                                                                                                                             Score 437.6; DB 36;
Pred. No. 9.2e-112;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodr.
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Si
Clone distribution: NCI-CGAP clone distribution in
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
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Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 496)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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On Nov 29, 1993 this sequence version
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note-"Organ: prostate; Vector: pAMP10; mRNA made from invasive prostate tumor, cDNA made by oligo-dT primitig. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman
                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:997813"
/clone_lib="NCI_CGAP_Pr10"
/sex="male"
/tissue_type="invasive prostate tumor"
/lab_host="DH10B"
                                                                                                                                                                                        ocation/Qualifiers
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                                                                                                                      rel: (301) 496-1550
Email: Robert C
                                                                                                                                                                                                                                                                                                                                                                                                       AA861869 456 bp mRNA ak44a06.sl Soares_testis_NHT 3', mRNA sequence.
                                                                                                         Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Ben
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                                                                                                                                                      Contact: Robert Strausberg, Ph.D
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                www-bio.lln1.gov/bbrp/image/image.html
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Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                    Unpublished (1997)
On Sep 12, 1996 this sequence version replaced
                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
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Pred. No. 8.5e-111;
0; Mismatches 3;
                                                                                                                       Bento
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                                                                                                                                                        GCACTTCAAAATGCATAAACCTGTTACAATGTTGAAA 1
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AI568832.1
                                                AI568832 440 bp nth16906.x1 NCI_CGAP_Pr28mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD;
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1408786"
/clone_lib="Soares_testis_NHT"
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Pred. No. 4.9e-110;
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                                                                                                                                                 rel: (301) 496-1550
Email: Robert 7
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Unpublished (1997)
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Tissue Procurement: Michael J. Brownstein, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Feb 18, 1999
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="IMAGE:2118490"
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/dev_stage="adult"
/lab_host="DH10B"
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A_Geneseq_36:W2708
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Database: A_Geneseq_36:*
Database sequences: 188963
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Search time (sec): 185.540000
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Query: US-09-030-606-115
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-Q-/cgn2_1/USPTO_spool/US09030606/runat_24091999_171616_29804/app_query.fasta.1
-Q-/cgn2_1/USPTO_spool/US09030606/runat_24091999_171616_29804/app_query.fasta.1
-DB-A_Geneseq_36 -QFMT-fastan -SUFFIX=rag -GAPOP=12.000
-GAPEXT=4.000 -MINATCH-0.100 -LOOPEXT-0.000
-LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOPE-6.000 -DELEXT-7.000 -START1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-escore
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-stat -USER-US09030606
-NCPU-6 -ICPU-3 -WAIT -THREADS-1
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       Partial human 7-transmembrane r
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                                                                                                                                           Human HG38 protein. Human G-produman receptor tyrosine kinase (Gly33-Tiel34) truncated GDNF. (Arg32-Tiel34) truncated GDNF. (Arg32-Tiel34) truncated GDNF. Snake venom ancrod polypeptide. (Pro23-Lys37delAsn37-Tiel-134) t Human DP.75, a putative GDP dis Human ATF-2. New astrocyte-deri Glial cell line-derived neurotr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein encoded Translation of ORF 3 contg. E. Neuropeptide Y/Ppeptide Y/Ppanrz Drug resistance-associated programment of oncogene v-ros. New Xenopus Frazzled protein W657-11 HTm4 protein. New isolated mammul HTm4 protein. Antibody specific Porcine pancreatic elastase III Mouse ULIP-3 protein. New GAP-association protein. New GAP-association of the protein of the Mouse and the protein work GAP-association of the protein work GAP-association work GAP-association of the protein work GAP-association work GAP-association of the protein work GAP-associat
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Sequence of protein having hum
Partial human pseudocholineste
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alignment_block:
US-09-030-606-115 x W88307
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A_Geneseq_36:R38298
A_Geneseq_36:R79375
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Pi faces or patient samples

Solisclosure; Fig 7: 165pp; English.

This is the amino acid sequence of an O antigen flippase encoded

by the wzx gene of a gene cluster (see X06748) involved in the

biosynthesis of the Escherichia coli Oll1 O antigen. The protein

chas 12 transmembrane segments and has similarity in secondary

ctructure to other wzx gene products. The use of nucleic acid

molecules derived from particular assembly and transport genes,

particularly wbd (transferase), wzx (flippase) and wzy (polymerase)

genes, within O antigen gene clusters improves the specificity of

methods for the detection and identification of O antigens, e.g. in

testing food- or faecal-derived samples, or samples from patients.

The O antigen is a major virulence factor of enteropathogenic E.

coli strains that cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: W88307 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
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22-JUL-1997; AU-008162.
01-MAY-1997; AU-006545.
(UNSY) UNIV SYDNEY.
Reeves PR, Wang L;
WPI; 99-059669/05.
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Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O antigen; Olli
                                                                                                                                                                   216 GCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATTTCACCCAGACAG
                                                                                                                                                                                                                                     166 TTAACCCATCTCTGAACTGGTAGAAAAACATCTGAAGAGCTAGTCTATCA
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01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. coli O antigen flippase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O antigen; Ollī antigen; wzx gene; flippase; diarrhoea; haemorrhagic colitis; diagnosis.
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                                                                                                                                     47
                                                                                                                                                                                                   32 ....IleIleThrProLeuIleLeuAsnHisLeuGlyLysGlnSerTyrG
                                                                                                                                                                                                                                                                        21 IleGluGlnPheValAsnProIleCysIlePhe....
                                                                                              pIleAlaLysIleIleAlaGluGlnArgIleLeuSerAspLeuSerLysL
                              GGTT.....CTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATA
                                                                ....ValSerPheSerGlnLeuIleCysGlyGlyCysSerAlaTr
                                                                                                                                 ly..........AsnTrpIleLeuLeuIleThrIle.......
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1.465
50.588
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Percent Identity:
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112
111
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52
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28.235
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160
185
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Human
Human
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98

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SE E DAC Seg
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Quality:
Ratio:
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US-09-030-606-115 x P60096
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                                                                                                                         documentation_block:
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            R37441;
06-0CT-1993 (first entry)
Partial human pseudocholinesterase sequence encoded by FBChE12.
butylcholinesterase; acylcholine acylhydrolase; EC 3.1.1.8; psi-ChE;
pseudo-ChE; neurotransmitter; organophosphorus insecticide; OP-poison;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 36: 44pp: English.

Human cholinesterase-type proteins can be used for the prophylaxis or for the treatment of the effects of organophosphorous cpd. poisoning. Other uses include clinical detection of pseudocholinesterase deficiencies, elucidation of the active site topography and the AA sequence of ACRE for the development of rapid simple clinical methods to detect poisoning or disease-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUN-1991 (first entry) Sequence of protein having human cholinesterase (ChE) activity in clone FBChE12a.
Organophosphorous poisoning; therapy; prophylaxis; diagnosis; pseudocholinesterase deficiency.
                                                                                                                                                                                                                     131
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16-JUN-1986; 108189
18-JUN-1985; IL-075
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P60096;
                                                                                                          R37441 standard;
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RES & DEV
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1.809
54.839
                                                                                                          Protein; 255
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seq_documentation_block:
ID F60097; standard; Prot
AC P60097;
DT 27-JUN-1991 (first e
DE Sequence of protein h
DE activity.
KW Organophosphorous poi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant human gene encoding human pseudo-cholinesterase used to treat organo-phosphorus poisoning Claim 3; Columns 40 and 41; 34pp; English.

A CDNA library prepared from foetal brain mRNA was screened with degenerate probe pools based on the organophosphorus binding site cholinesterases. A 764 nucleotide insert (designated FBChEl2) was isolated from one positive clone and sequenced. This insert, containing an ORF large enough to code for about half the subunit size of human cholinesterase, was used as a probe to obtain the full ength pseudocholinesterase sequence. See also 042496.
                             Sequence of protein having human cholinesterase (ChE)
Organophosphorous poisoning; therapy; prophylaxis; diagnosis;
                                                                                                                                                                                                                                                      108
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peptide
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18-JUN-1986; US-875737.
21-AUG-1987; US-087724.
15-AUG-1990; US-572911.
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                                                                                                                                                                                                                                                  IleSerProLysTyrTyrMetIlePheThrProCysLysLeu.....
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Ratio:
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                                                (first entry)
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101. .110
/note= "shown in the specification as being encoded by the sequence TCT CTG ACC AGG TGG TCT GAT ATT TGG ACT which should correspond to the amino acid sequence SITRWSDIWT"
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1.809
54.839
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                                                                               Protein; 635
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seq_documentation_block:
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzyme claim 17; Page 38-40; 44pp; English.
Claim 17; Page 38-40; 44pp; English.
Human cholinesterase-type proteins can be used for the prophylaxis or for the treatment of the effects of organophosphorous cpd.
poisoning. Other uses include clinical detection of pseudocholinesterase deficiencies, elucidation of the active site topography and the AA sequence of AChE for the development of rapi simple clinical methods to detect poisoning or disease-related to the company of the sequence of AChE for the development of the simple clinical methods to detect poisoning or disease-related to the company of the sequence of AChE for the development of the simple clinical methods to detecting mutations in ChE genes.
                                                                                                                                                                                   Full-length foetal human pseudocholinesterase. butylcholinesterase; acylcholine acylhydrolase; pseudo-ChE; neurotransmitter; organophosphorus i
                                                                                                                                                                                                                                                      R41509 standard;
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                                                                                                                                                             Homo sapiens.
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18-JUN-1985;
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  /note=
403..4
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/note= "potential
303. .305
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1.779
54.839
                                          /note-
                                                                                            /note-
                                                                                                                                              ocation/Qualifiers
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                                                                                                                      note-
"potential N-glycosylation s. 18. .320 ote= "potential N-glycosylation s. 1. .405
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58
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                                                                                                                    "putative leader peptide"
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                                                                                            "potential
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Gaps: 5
Percent Identity: 29.032
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                N-glycosylation site"
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seq_documentation_block:
ID R24297 standard; Prot
AC R24297;
DT 20-NOV-1992 (first e
DE Glycopeptide resistan
KW Gycopeptide antibiot
KW D-Ala-D-Ala ligase; p
KW Inverted repeats.
OS Enterococcus faecium
PN W09207942-A.
PD 14-MAY-1991; F00855.
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US-09-030-606-115 x R41509
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to treat organo-phosphorus poisoning
Claim 4; Columns 41-46; 34pp; English.
A cDNA library prepared from foetal brain mRNA was screened with
degenerate probe pools based on the organophosphorus binding site of
cholinesterases. A 764 nucleotide insert (designated FBChE12) was
isolated from one positive clone and sequenced. This insert (Q42495),
containing an ORF large enough to code for about half the subunit
size of human cholinesterase, was used as a probe to obtain the full-
length pseudocholinesterase sequence by screening a foetal liver
cDNA library and a primary glioblastoma cDNA library (Q48393).
This sequence differs from sequence Q42496, particularly in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1993.
18-JUN-1986;
18-JUN-1986;
18-JUN-1987;
15-AUG-1990;
15-AUG-1990;
YEDA YEDA
                                                                     Glycopeptide resistance protein VanH Glycopeptide antibiotic; vancomycin; D-Ala-D-Ala ligase; peptidoglycan pre
                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                          8 CTCTCCCCTCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATT
                                                                                                                                                                                                                                                                                                                                                                 IleSerProAsnTyrTyrMetIlePheThrProCysLysVal.....
                                                                                                                                                                                                                                                  AATCCATCTTGCTTTTTCCCCCATTGGAACTAGTCAT
                                                                                                                                                                                                                                                                           etHisSerLysValThrIleIleCysIleArgPheLeuPheTrpPheVal
                                                                                                                                                                                                                                                                                                        TGTTT...AAAATTACT.............
                                                                                                                                                                                                                                                                                                                                      ...LeuLeuCysMetLeu...
                                                                                                                                                                                      A_Geneseq_36:R24297
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US-875737.
US-087724.
US-572911.
                                                                                                                     (first entry)
                                             faecium BM4147
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543. .:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.50
1.779
54.839
                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "active site serine"
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Percent Identity:
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0:
                                                                      anH from E.faecium.
in; teicoplanin; resisi
precursor; transposon.
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29.032
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polympitides involved in expression of glycopeptide antibiotic resistance - useful in diagnosing presence of Gram-positive enterococcal strains e.g. Enterococcus faecium and E gallinarum Stalin 1; Fig 8; 163pp; French.

C Laim 1; Fig 8; 163pp; French.

C Laim 1; Fig 8; 163pp; French.

C VanH is coded for by a 7.3kb Hindill-EcoRI fragment of the plasmid plassid. (The plasmid contains resistance genes from Enterococcus faecium BM 4147 and was described in New England J.

C Med., 319:157-161). The VanH protein has a mol. mass of 35,754 and that similarities to dehydrogenases which catalyse NAD+ dependent coxidation of 2-hydroxycarboxylic acids. VanH interacts with VanA, a D-Alanine:D-Alanine ligase. Resistance to glycopeptides is thought to involve the blosynthesis of a new component by VanA; the new peptide can be incorporated with peptidoglycans but is not recognised by vancomycin. See also Q25178-Q25183.
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AU9050726-A.
13-SEP-1990.
06-MAR-1990;
07-MAR-1989;
29-MAY-1989;
                                                                                                                                                R07507;
07-FEB-1991 (first entry)
Murine IL-2R beta chain.
Interleukin; receptor.
                                                                                                                                                                                                                                                                                                                                                                     212
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(INSP ) INST PASTEUR.
Arthur M. Courvalin P. Dutka-malen
WPI: 92-183677/22.
                                                                                                 misc_difference
                                                                                                                                  Mus
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                                                                                                                                                                                                                 R07507 standard;
                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                musculus.
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                                                                                                                                                                                                                                                                                                                                                                   eSerHisGlu......GlnI
                                                                                                                                                                                                                                                                                                                                                                                                  GCAACACAATATACATCACAGTGAAATGTGTAATCCTTGCAAATTGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                 AspIleValThrLeuHisValProLeuAsnThrAspThrHisTyrIleIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlyThrGlyGlnIleGlyLysAlaValIleGluArgLeuArgGlyPh
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                                                                                                                                                                                                                                                                                                leGlnArgMetLys 221
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050726.
EP-104023.
EP-109656.
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                                                                                                 Location/Qualifiers 231
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1.250
54.545
                                                                                  /label=G,
                                                                                                                                                                                                               protein;
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seq_documentation_block:
ID W73405
AC W73405
DT 19-FEB-1999 (first e
DE Human secreted protein; hum
KW pathological condition
KW developmental abnorma
KW immune system disorde
KW schizophrenia; prosta
OS Homo sapiens.
FH Key
FT Misc_difference 287
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US-09-030-606-115/rev x R07507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                        Human secreted protein encoded by Gene No. 9.

Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; protein therapy; gene therapy; blood disorder; pathological condition; disposis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepd. from RNA extracted from Concanavalin A-stimulated mouse spleen cells. The clones were selected using a probe derived ithe human sequence. The sequence encodes a soluble portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis and therapy by immune suppression Claim 4; Fig 8; 65pp; English.
The sequence was obtd. from clones isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taniguchi T, Hatakeyama M, Minamoto
Miyasaka M, Tsudo, Karasuyma H;
WPI; 90-327673/44.
                                                                                                                                                                                                                                                                                                                                   374 nAlaLeuGluIleGluSerCysGlnValTyrPheThrTyrAspProCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 CATGTAGAGAACCCAAACTAATTTATTAAACAGGATAGAAACAGGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; Q06332.

Recombinant interleukin-2 receptor beta chain - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                346 pSerAlaProLeuProSer.ProSerGlyHisSerGlnAlaSerCysPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 CTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 euSerPhePheSerProSerGlyProAlaProGluIleSerProLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 HisIleProAspProSerGluPhePheSerGln.....LeuSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The human sequence. IL-2R beta chain.
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(BOEH ) BOEHRINGER INGELHEI.
                                                                                                                                                                                                      19-FEB-1999 (first entry)
                                                                                                                                                                                                                                           W73405 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                       79 TATACATCACAGTGAAATGTGT......AATCCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCAAGATGGA...TTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValLeuAspGlyAspSerLysAlaValGlnLeuLeuLeuCeuClnLysAs
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                                      Location/Qualifiers 221
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1.132
                     'note-
                     "unspecified amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                             .GlyTyrPhePhePheHisLeuProAs
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alignment_scores:
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CC conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a cC sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal cegnitive disorders, blood disorders, leukaemias, diseases of the immune system cC conditional and alergies or asthma), hepatic disease, Alzheimer's and cC cognitive disorders, schizophrenia, prostate diseases, autoimmune cC disorders and AIDS. The polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: W73405
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-030-606-115 x W73405
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03-DEC-1998.
28-MAY 1998; U10868.
29-AUG-1997; US-056296.
30-MAY 1997; US-044039.
30-MAY 1997; US-0448191.
30-MAY 1997; US-0448190.
30-MAY 1997; US-048190.
30-MAY 1997; US-048190.
30-MAY 1997; US-048190.
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Carter KC, Dillon PJ, Endress GA, Feng P,
                                                                                                                          170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1997; US-056250.
29-AUG-1997; US-056293.
                                        220 CTGACAGGTGAATTGGATGGTTCTCAGAACCATTTCACCCAGACAGCCTG
    52
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eH1sSerIleAsnTyrTyrPheIleAsnSerGlnGlyPro.....
                                                                                                                                                            isTrpLeuMetAlaAlaLeuAlaPhe............
                                                                                                                                                                                                      CTTGGTTTGTGAATCCATCTTGCTTTTTCCCCATTGGAACTAGTCATTAA 169
                                                                                                                                                                                                                                          pValSerIleLeuCys.....ArgAsnThrTyrSerValPheLysIleH 36
                                                                                                                                                                                                                                                                                  GTGATGTATTGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTA 119
                                                                                                                                                                                                                                                                                                                        LeuTyrMetValMetSerAlaCysPheLeu...AlaAlaGlyIlePheTr
                                                                                                                                                                                                                                                                                                                                                                 CTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACT
                                                                                                                      CCCATCTCTGAACTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCAT
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1.204
44.954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
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                                                                              ..ThrLysSerIleSerLeuLeuPh
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6
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seq_documentation_block:

ID R24307; standard; Protein; 2408 AA C R24307;

DT 20.NOV-1992 (first entry)
DE Translation of ORF 3 contq. Efae KW Glycopeptide antibiotic; vancomyc KW D-Ala-D-Ala ligase; peptidoglycan KW Open reading frame.

OS Enterococcus faecium BM4147.
EH Key Location/Qualifie FT /Abbel- VanH /Oote- "see R2429 PN W9207942-A.
FT W09207942-A.
PD 14-MAY-1992.
PR 31-OCT-1991; F00855.
PR 31-OCT-1991; F00855.
PR 31-OCT-1990; FR-013579.
PA (INSP) INST PASTEUR.
PI Arthur M, Courvalin P, Dutka-male N-PSDB; Q251837
PT polypeptides involved in expressi PT resistance - useful in diagnosing PT resistance - useful in diagnosing PT resistance - useful in diagnosing PT enterococcal strains e.g. Enteroc PS Disclosure; Fig 5; 163pp; French.
CC A 7.3kb fragment of E.faecium DNA CC vanA, vanX, vanR and vanS involved translated in each of the three p CC sidicate the position of nonsense See also Q2518-Q2582.
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    Quality:
    Ratio:
    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                          1339 ValGlyThrGlyGlnIleGlyLysAlaValIleGluArgLeuArgGlyPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q25183.

Polypeptides involved in expression of glycopeptide antibiotic resistance - useful in diagnosing presence of Gram-positive enterococcal strains e.g. Enterococcus faecium and E gallinarum Disclosure; Fig 5; 163pp; French.

A 7.3kb fragment of E.faecium DNA containing the five genes vanH, vanA, vanX, vanR and vanS involved in antibiotic resistance was translated in each of the three possible open reading frames. Within ORF 3 were the vanH and vanX genes. The "X"s in the sequence indicate the position of nonsense codons.

See also Q25178-Q25182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1992 (ILIST ENGL) E.faecium proteins vann and Translation of ORF 3 contg. E.faecium proteins vann and Glycopeptide antibiotic; vancomycin; teicoplanin; resist; D-Ala-D-Ala ligase; peptidoglycan precursor; transposon; D-Ala-D-Ala ligase; vanR: vanR; vanR; vanR; vanR; vanR; vanR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1991; F00855.
31-OCT-1990; FR-013579.
(INSP ) INST PASTEUR.
Arthur M, Courvalin P, Dutka-malen S, Molinas
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                                                                                                                                                                                                                                                                                                                                                              276 ATAGAAACAGGCTGTCTGGGTGAAATGGTTCTGAGAACCATCCAA...TT
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                                                rgSerIleGluValAsnTyrValProPheAspGluLeuLeuGlnAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTGCTCCAATCTGTCACATAAAAGT
AspIleValThrLeuHisValProLeuAsnThrAspThrHisTyrIleIl 1399
                                                                                                                                                     CAGAGATGGGTTAATGACTAGTTCCAATGGGG.....AAAAAGCAA 139
                                                                                                                                                                                                      eGlyCysLysValLeu.....AlaTyrSerArgSerA
                                                                                                                                                                                                                                                          CACCTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTT 180
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1.250
54.545
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1842. .2056
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Gaps: 4
Percent Identity: 25.000
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                                                      89
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seq_documentation_block:
ID R79120 standard; Prot
AC R79120;
C R79120 standard; Prot
AC R79120 standard; Prot
AC R79120;
C STANDARD STANDARD STANDARD
AC R79120 standard; Prot
AC R79120; Special Special Standard; Prot
AC R79120; Special Standard; Prot
AC R79120; Special Specia
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                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
122 sMetSerValThrValSerIleLeuSerLeuValLeuValAlaLeuGluA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1995.
28-DEC-1994; U14436.
28-DEC-1993; US-176412.
(SYNA-) SYNAPTIC PHARM C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; 094172.
New nucleic acid encoding a Y4-Receptor, New nucleic acid for treating amnesia, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a rat neuropeptide Y/peptide YY/pncretic polypeptide (Y4) receptor, which can be used to screen drugs which bind to it, specifically to find ligands (agonists or antagonists) which bind to it. The ligands can be used to treat abnormalities, specifically the antagonists can be used to treat amnesia, feeding disorders, epilepsy, hypertension, sleeping disorders or pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bard JA, Branchek T, Walker MW, WPI; 95-246190/32.
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Neuropeptide Y/peptide YY/pancretic polypeptide receptor (Y4).
Y4 receptor; hp25a neuropeptide receptor; antisense oligonucleotide;
                                                                                                             109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or epilepsy, etc.
Disclosure; Fig 3; 154pp; English.
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                                             83 TGTTGCAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAA 132
                                                                                                                                                           33 TTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTG
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                                                                                                       PheGlyGluValLeuCysLysMetLeuThrPhe.....IleGlnCy
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                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                       R79120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "tı
212. 235
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118. .137
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                                                                                                                                                                                                                                                                                                                                                        58.00
1.349
51.190
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                                                                                                                                                                                                                                                                                                                                                        Length: 84
Gaps: 5
Percent Identity: 29.762
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                        alignment_block:
                                                                                                    Align seg 1/1 to: W00215 from: 1
                                                                                                                                      US-09-030-606-115 x W00215
                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                      New gene encoding protein kinase involved in multiple drug
resistance - potentially useful as cyto-protectant and target for
reversing drug resistance in cancer cells

Claim 4; Page 33-36; 57pp; English.

The amino acid sequence (W00215) of a C-terminal portion of a
membrane-associated serine-threonine protein kinase, designated
pKR, was deduced from a cDNA clone (T33370) obtd. from MDR human
cell line KB-V1. The novel kinase has higher activity in several
CMDR cell lines than in sensitive parental cells. It is also
cexpressed at high activity in the brain. It may be important in
the pathway leading to MDR. Inhibition of the kinase may
therefore re-sensitise cells to chemotherapeutic drugs. Should
pKR have a role in stress control, then inhibition might lead to
cedath of resistant tumour cells. Variant PKR proteins can be
produced in which PKR amino acids are replaced by similarly
sequence 1160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _documentation_block:
W00215 standard; Pro
                                  663 ArgProArgSerSerPheLeuArgArgProLeuValGluHisArgGlnMe 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1996; U02375.
28-FEB-1995; US-396399.
(PHAA ) PHARMACIA & UPJOHN CO.
Abzaham I, Begley DA, Sampso
WPI; 96-412781/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key Location/Qualifiers
misc_difference 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drug resistance-associated protein kinase. Protein kinase; PKR; multi-drug resistance; MDR; cancer; tumour; chemotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 TG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 lIleTrpPheIleSerCysPheLeuSerLeuProPheLeuAlaAsnSerI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 TrpLysProSerIleSerGlnAlaTyrLeuGlyIleVal......Va
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06-SEP-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T33370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1996 (first entry)
                                                                91 AAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAAT
GCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTC....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGATGGTTC........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein;
                                                                                                                                                                                       57.50
1.127
47.222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "the sequence given on beyond stop codon-1161"
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                                                                                                                                                                                       Percent Identity:
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                                                                                                    to: 1160
                                                                                                                                                                                       108
5
26.852
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184
                                                                    140
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seq_documentation_block:
ID p60007 standard; Prot
AC p60007;
DT 30-JUL-1991 (first e
DE Sequence of oncogene
KW Therapy; diagnosis; 1
PN EP-19292-A.
PP 10-FEB-1986; 300894.
PR 12-FEB-1986; US-70077
PA (GETH ) GENENTECH INC
PI Bell JR, Ulrich A, Ra
DR WPI; 86-225966/35.
PT New DNA encoding insu
PT synthesis of receptor
Se Example; Fig 5; 62pp;
CC A mutant IR is claime
CC the precursor process
by deletion of the tr
CC activity may be inact
CC domain of the insulin
SQ Sequence 278 AA;
                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-030-606-115/rev x P60007
seq_documentation_block:
ID W97634 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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                                                          seq_name: A_Geneseq_36:W97634
                                                                                                                                                                                                                                                                                            Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example: Fig 5: 62pp; English.

A mutant IR is claimed which may have a mutated alpha-chain, esp. at the precursor processing site. The beta-chain may be mutated, e.g. by deletion of the transmembrane sequence; the tyrosine kinase activity may be inactivated. Fig. 5 is a comparison of oncogene and human EGF receptor sequences with that of HIR in the cytoplasmic domain of the insulin receptor beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1986.
10-FEB-1986; 300894.
12-FEB-1985; US-700776.
12-FEB-1985; US-700776.
GETH ) GENENTECH INC.
Bell JR, Ulrich A, Ramachandran J;
WPI; 86-226966/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695 hrThrLeuThrSerGluSerValAlaGlySerHisArgLeuGlyAsp.Tr 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of oncogene v-ros. Therapy; diagnosis; insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  728 roLeuLeuThrAsnGlnIleThrLeuSerAlaProGlnProValSerVal 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235
                                                                                                                                                                                                   255 AsnArgProThrPhePheTyrIleGlnHisLysLeuGlnGluIleArgHi
                                                                                                                                                                                                                                           111 AACAAAGACACTTTTTTTTTTTTGCAACAC.....AATATACATCA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA encoding insulin receptor or its fragments - used for synthesis of receptor and mutants for therapeutic and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761 sGlnCysGlnAsnArgSerAsn 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 ACCCTGCTCCAATCTGTCACAT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 GlyIleAlaH1sValValTrpProGlnProAlaThrThrLysLysAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 GTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tLeuValProAlaTrpGln...GlnValThrProLeuAlaProAlaThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pGlyLysMetIleSerCysSerAsnHisTyrAsnSerValMetProGlnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTTTAATAAATTAGTTTGG......GTTCTCTACATGCATAACAA 318
                                                                                                           sSerProLeuCys 275
                                                                                                                                                     CAGTGAAATGTGT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AGAACCATTTCACCCAGACAGCCTGTTTCTATC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_36: P60007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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3.531
76.190
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Gaps: 1
Percent Identity: 47.619
  281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
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seq_documentation_block:
ID w06503 standard; Pro-
AC w06503;
DT 06-FEB-1997 (first of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
                                                                                                                                seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Critical Sequence of novel xenopus frazzled protein (W667-16, as deduced from an isolated cDNA clone (see X06998). The Crimothion provides Xenopus W667-16, W667-19 and WA628-5 polypetides (see W98634-36), isolated DNA molecules (see X06998-700), vectors, conditions are used: to modulate regulation of pancreatic genes (e.g. for pancreatic tissue repair and for treatment or combinant protein production. Prazzled proteins are used: to modulate regulation of pancreatic clasue repair and for treatment or combinate cell development (particularly in haematopoletic gut, concluding inducing de novo formation of beta-1slet cells); to modulate cell development (particularly in haematopoletic gut, concluding inducing particularly for inducing cell formation, growth, conditate cell development (particularly for inducing cell formation, growth, condition of chondrocytes and/or cartilage tissue by treating progenitor cells in vitro; generally to modulate effect of wnt cents; to raise antibodies; and as dietary supplement or cell culture additive. They are also used: to treat diseases associated the activities, e.g. in wound healing; to treat or prevent rheumatoid arthritis, osteoarthritis or other articular cartilage disorders; in combination with transplants of cells for treating neuronal conditions and to induce formation of hormone-producing cells, in both human and veterinary medicine.

Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: W97634 from:
                                                                                                                                                                                                                                                                                                                                                                                              US-09-030-606-115/rev x W97634
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w97634;
10-MAY 1999 (first entry)
Xenopus Frazzled protein WG67-16.
Yenopus Frazzled; wG67-16; cell growth; cell differentiation;
cell proliferation; wound healing; vulnerary; tissue repair;
pancreatitis; diabetes; rheumatoid arthritis; osteoarthritis;
chondrocyte; cartilage; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; X06998.

New DNA encoding Frazzled proteins - for modulating growth, differentiation, proliferation of cells, e.g. in treatment of wounds, diabetes and rheumatoid arthritis claim 3; Page 44-45; 71pp; English.
                                                                                                                                                                                                                                                              234 LysLeuIleArgAsnArgProThrValTyrValIleAlaGlyAspIleHi 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
LAVALLIE ER, Paulsen J, Racie L, Sive H, Sun
WPI; 99-120880/10.
                                                                                                                                                                        250 sHisGlyLysIleLysIlePheCysSerProCysValLeuArg 264
                                                                                                                                                                                                                                                                                                         123 CAAGTAATTTTAAACAAAGACACTTTTTTTTTTTTTGCAACACAATATACA 74
                      06-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1999.
28-APR-1998; U08517
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                                                                   W06503 standard; Protein; 214 AA
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                                                                                                                                                                                                                   73 TCACAGTGAAATG......TGTAATCCTTGCAAATTGCAA 40
                                                                                                                           A_Geneseq_36:W06503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
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2.690
67.742
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32.258
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seq_documentation_block:
ID W41056 standard; Pr
'AC 'W41056;
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                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                            US-09-030-606-115/rev x W06503
                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
   W41056 standard; Protein;
'W44056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents human HTm4 protein. HTm4 is related to the FC(epsilon)RI receptor (FR). HTm4 contains four hydrophobic domains of 20-21 maino acids. The N-terminal region before the first hydrophobic domain contains four proline residues, and each of the hydrophilic regions between the hydrophobic regions contains one proline. This protein crosses the plasma membrane four times forming two small extracellular loops and has both the N- or C-terminals in the cytoplasm. The HTm4 gene and protein can be used in the research and study of the induction of expression of FR and the function of its subunits. They can be used in the design of drugs which can block or inhibit induction of FR, thereby treating atopic diseases such allergy, asthma, atopic dermatitis and allergic rhinitis. The HTm4 gene sequences may also be used to detect patients suffering thromesome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5552312-A.
03-SEP-1996.
06-OCT-1994;
06-OCT-1994;
                                                                                                                                                                                                                                                   206
                                                                                                                                                                                      159
                                                                                                                                                                                                                                                                                                         253 AATGGTTCTGAGAACCATCCAATTCACCTGTCA...GATGCTGATAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated mammalian HT(M4) protein DNA - used to develop prods. for use in the diagnosis and treatment of atopic diseases, e.g. allergy or asthma Claim 2; Fig 1; 10pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BETH ) BETH ISRAEL HOSPITAL BOSTON
Adra CN, Lelias J, Lim B;
WPI; 96-412066/41.
N-PSDB; T45120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human HTm4 protein; Fc(epsilon)RI receptor; I allergic asthma; atopic dermatitis; allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                       63
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                                                                                            79
                                                                                                                                                                                                                                                                                  30
                                                                                        CAAAGACACTTTTTTTTTTTGCAACACAATATACA 74
                                                                                                                                                                                                                                                                             euAlaLeuGlyValPheLeuGlySerLeuGlnTyrProTyrHisPhe...
                                                                                                                                                                                    GTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTTTAAA 110
                                                                                                                                                                                                                     aLysLeuGlnValLeuGlyAlaIleGlnIleLeuAsnAlaAlaMetIleL
                                                                                                                                                                                                                                                  AGCTCTTCAGATGTTT...TTCTACCAGTTCAGAGATGGGTTAATGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 AA;
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US-318492.
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173. .:
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                                                                                                                                                                                                                                                                                                                                                                                                                        56.00
1.556
58.065
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                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Transmembrane
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                B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain'
                                                                                                                                                                                                                                                                                                                                                                                                                        37.097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FR; atopic rhinitis;
                                                                                                                                                                                                                     63
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hereditary.
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alignment_block:
US-09-030-606-115/rev x W41056
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody specific for HTm4 protein - useful to block or mimic ligand binding or detect haematopoletic cells Disclosure; Column 25-28; 18pp; English.

This sequence is the HTm4 protein. The HTm4 protein is specifically bound by the antibody of the invention. HTm4 shows homology to the beta subunit of the high affinity IgE FC receptor (FcepsilonRibeta) and the CD20 antigen, both of which are in the 4-transmembrane spanning proteins superfamily (TM4SF). The antibody of the invention is used to block or mimic binding of ligands such as the tumour necrosis factor (TNF) receptor-associated factors TRAF-1, TRAF-2 and TRAF-3 and the phosphatase, CDK-activating kinase (KAP), to receptors comprising HTm4, and to detect haematopoletic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTm4 protein.

HTm4; antibody; IgE Fc receptor; FcepsilonRIbeta; CD20 antigen; TRA 4-transmembrane spanning protein superfamily; ligand binding mimic; haematopoietic cell detection; inhibitor; transmembrane and detection; inhibitor; transmembrane and make a constructions of the construction of the constru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adra CN, Lelias J, Lim WPI; 98-086194/08.
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03-JUL-1996;
                                                                                                      109 CAAAGACACTTTTTTTTTTTTGCAACACAATATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 AGCTCTTCAGATGTTT...TTCTACCAGTTCAGAGATGGGTTAATGACTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V03875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-APR-1998
                                                                                                                                                                                                      63 euAlaLeuGlyValPheLeuGlySerLeuGlnTyrProTyrHisPhe...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aLysLeuGlnValLeuGlyAlaIleGlnIleLeuAsnAlaAlaMetIleL
GlnLysHisPhePhePhePhe...ThrPheTyrThr
                                                                                                                                                                                                                                                                                                                             GTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTTTAAA
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Query: US-09-030-606-115
Query length: 366
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-0-/cgn2_1/USPTO_spoo1/US09030606/runat_24091999_171616_29813/app_query.fasta.1
-DB-Issued_Patents_AA -QFMT-fastan -SUFFIX-rai -GAPOP-12.000
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sequences: 106577
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                        Percent Similarity:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION UNUBER: US/08/286,819A
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
                                                                                                TELEFAX: (703) 413-22: TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5871910man F
REGISTRATION NUMBER: 24,718
REFERENCE/DOCKET NUMBER: 660-
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
                                                                             SEQUENCE CHARACTERISTICS
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MOLECULE TYPE:
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    TOPOLOGY: 14---
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                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FR 9013579 FILING DATE: 31-OCT-1990
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US-09-030-606-115/rev x US-08-286-819A-2
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TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
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FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
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         PRIOR APPIICATION DATA:
                                                                        PRIOR APPLICATION DATA:
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                         APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1991
                                                                                                                                                                                   FILING DATE: 21 CLASSIFICATION:
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MOLINAS, CATHERINE
COURVALIN, PATRICE
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                                                                                                                                                                                                                                                                                                                      US/08/286,819A
                                                 PCT/FR/91/00855
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US-09-030-606-115/rev x US-08-286-819A-29
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Percent Similarity:
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Sequence 28, Application PC/TUS9414436
GENERAL INFORMATION:
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TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 ATAGAAACAGGCTGTCTGGGTGAAATGGTTCTGAGAACCATCCAA...TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 CAGAGATGGGTTAATGACTAGTTCCAATGGGG......AAAAAGCAA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 CACCTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 5871910
                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 31-OCT CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Oblon, NO. 5871910man REGISTRATION NUMBER: 24,618
                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGAAAGAATTAAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eSerHisGlu......GlnI 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAACACAATATACATCACAGTGAAATGTGTAATCCTTGCAAATTGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                      E: Cooper & Dunham
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2291 amino acids
                                                                                                                                                   Weinshank, Richard L.

VENTION: DNA ENCODING A HUMAN NEUROPEPTIDE YY/PANCREATIC POLYPEPTIDE YY/PANCREATIC POLYPEPTII Y/PANCREATIC POLYPEPTII Y/PANCREATIC POLYPEPTII Y/PANCREATIC POLYPEPTII Y/PANCREATIC POLYPEPTION (Y4) AND USES THEREOF
                                                                                                                                                                                                                                                                     Walker, Mary
                                                                                                                                                                                                                                                  Branchek, Theresa
                                                                                                                                                                                                                                                                                               Bard, Jonathan A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1990
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1.250
54.545
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Gaps: 4
Percent Identity: 25.000
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alignment_block:
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                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-318-492-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: PCT-US94-14436-28 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-030-606-115 x PCT-US94-14436-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                Sequence 4, Application US/08318492 Patent No. 5552312
                                                                                                                                                          GENERAL INFORMATION:
    APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: RECOMBINANT HTM4 GENE, PROTEIN AND
TITLE OF INVENTION: ASSAYS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 rgHis......GlnLeuIleIleAsnProThr...Gly 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 TCCATCTTGCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAAC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 44743-A-PCT\JPW\MAT TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                         179 le 179
                                                                                                                                                                                                                                                                                                                                                                                                                       162
                                                                                                                                                                                                                                                                                                                                                                                                                                           233 TGGATGGTTC......TCAGAACCATTTCACCCAGACAGCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 TGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 sMetSerValThrValSerIleLeuSerLeuValLeuValAlaLeuGluA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 PheGlyGluValLeuCysLysMetLeuThrPhe.....IleGlnCy 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-LOSS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14436
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                     268 TG 269
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 TGTTGCAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTTGTGAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                lIleTrpPheIleSerCysPheLeuSerLeuProPheLeuAlaAsnSerI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpLysProSerIleSerGlnAlaTyrLeuGlyIleVal.....va 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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1.349
51.190
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5
29.762
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; LENGTH: 214 amino ac:
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-492-4
                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-707-340-4
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US-09-030-606-115/rev x US-08-318-492-4
                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                 Sequence 4, Application US/08707340 Patent No. 5705615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Relicurrent APPLICATION DATA: APPLICATION NUMBER: US
                       NUMBER OF SEQUENCES: 4
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                         APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: RECOMBINANT HTM4
TITLE OF INVENTION: ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: BI TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                              109 CAAAGACACTTTTTTTTTTTTGCAACACAATATACA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 GTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTTTAAA 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 AATGGTTCTGAGAACCATCCAATTCACCTGTCA...GATGCTGATAGACT
                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 euAlaLeuGlyValPheLeuGlySerLeuGlnTyrProTyrHisPhe...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 AsnThrSerValTyrHisProIleAsnGlySerProAspTyrGlnLysAl 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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1.556
58.065
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                                            Smith & Reynolds, P.C
                                                                                                                                     GENE, PROTEIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
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STATE: N

Massachusetts

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-707-340-4
                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-030-606-115/rev x US-08-707-340-4
                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-916-902A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-707-340-4 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                 Sequence 3, Application US/08916902A Patent No. 5871930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: BH19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,492
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/675,648
APPLICATION NUMBER: US 08/675,648
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                         APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HIGH AFFINITY IMMUNOGLOBULIN E
TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 AGCTCTTCAGATGTTT...TTCTACCAGTTCAGAGATGGGTTAATGACTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 AATGGTTCTGAGAACCATCCAATTCACCTGTCA...GATGCTGATAGACT 207
                                                                                                                                                                                                                                                                                                                                                                                                109 CAAAGACACTTTTTTTTTTTTGCAACACAATATACA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 GTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTTTAAA 110
ORRESPONDENCE ADDRESS:
                                                                                                                                                APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                  63 euAlaLeuGlyValPheLeuGlySerLeuGlnTyrProTyrHisPhe... 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 AsnThrSerValTyrHisProIleAsnGlySerProAspTyrGlnLysAl 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 aLysLeuGlnValLeuGlyAlaIleGlnIleLeuAsnAlaAlaMetIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01 FILING DATE: 03-SEP-1996
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1.556
58.065
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Gaps: 4
Percent Identity: 37.097
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alignment_block:
US-09-030-606-115/rev x US-08-916-902A-3
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                                                                                                                                                                   seq_documentation_block:
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Sequence 2, Application:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GAP-Associated Protein p190 and
TITLE OF INVENTION: Transduction
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-916-902A-3 from: 1 to: 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatib
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for I
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AGCTCTTCAGATGTTT...TTCTACCAGTTCAGAGATGGGTTAATGACTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AATGGTTCTGAGAACCATCCAATTCACCTGTCA...GATGCTGATAGACT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                 109 CAAAGACACTTTTTTTTTTTTGCAACACAATATACA 74
                                                                                                                                                                                                                                                                                                                                                                                      159 GTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTTTAAA 110
                                                                                                                                                                                                                                                      79 GlnLysHisPhePhePhePhe...ThrPheTyrThr 89
                                                                                                                                                                                                                                                                                                                                           63 euAlaLeuGlyValPheLeuGlySerLeuGlnTyrProTyrHisPhe...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 AsnThrSerValTyrHisProIleAsnGlySerProAspTyrGlnLysAl 46
                                                                                                                                                                                                                                                                                                                                                                                                                              46 aLysLeuGlnValLeuGlyAlaIleGlnIleLeuAsnAlaAlaMetIleL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: Herewi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: GenBank CLONE: 561639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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FastSEQ for Windows Version
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1.556
58.065
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37.097
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alignment_scores:
    Quality:
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                                                           seq_documentation_block:
Sequence 1, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                            seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-564-458-1
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-030-606-115 x PCT-US93-03076-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: PCT-US93-03076-2 from: 1
                                          Patent No. 5641749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-801-914
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE TARACTERISTICS:
1.FNGTH: 1513 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03076
FILING DATE: 19930331
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          855 rIleValPheTyrSerAlaLysArgLysAlaSerLeuAlaMetLeuArgA 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
                                                                                                                                                                                                                254
                                                                                                                                                                                                                                                          905
                                                                                                                                                                                                                                                                                                  207
                                                                                                                                                                                                                                                                                                                                            688
                                                                                                                                                                                                                                                                                                                                                                                      169
                                                                                                                                                                                                                                                                                                                                                                                                                            872 laPheLeuCysGluValGlnAspIleIleProIleGlnLeuValAlaLeu 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 ACTTGGTTTGTGAATCCATCTTGCTTTTTCCCCCATTGGAACTAGTCATTA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2 Milit:
CITY: Lexington
STATE: MA
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REFERENCE/DOCKET NUMBER: WHI92-03A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                 uThrGluGlyGluGluIleAlaGlnGluIleAspGly.....ArgP 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACCCAGACAGCCTGTTTCTATCCT 279
                                                                                                                                                                                                                                                                                                                                          ThrAspGlyAlaIleAspValLeuAspAsnAspLeuSerArgGluGlnLe 905
                                                                                                                                                                                                                                                                                                                                                                                  ACC.....CATCTCTGAACTGGTAGAAAAACATCTGAAGAGCT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGATGTATATTGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCAC
                                                                                                                                                                                                                                                                                              AGTCTAT...CAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATT 253
                                                                                                                                                                    heThrSerIleProCysSerHisPro 927
                      INFORMATION:
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                                                       Application US/08564458
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Yan, Qiao
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1.056
58.696
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; NAME/KEY:
US-08-564-458-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                           Sequence 1, Application US/08564833 Patent No. 5641750
                              GENERAL INFORMATION:
APPLICANT: Louis, Jean-Claude
APPLICANT: Louis, Jean-Claude
TITLE OF INVENTION: Methods for Treating Photoreceptors Using Glial Cell
TITLE OF INVENTION: Line-Perived Neurotrophic Factor (GDNF) Protein
TITLE OF INVENTION: Product
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acid residues
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ITTLE OF INVENTION: ITTLE OF INVENTION: INVENTION: INVENTION: ITTLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: 805-447-8102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CURRY, Daniel R.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 TAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGG
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                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 ATCTTGCTTTTTCCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           236 ATGGTTCTCAGAACCATTTC 255
                                                                                                                                                                                                                                                                                                               73 spalaalaGluThrThrTyr 79
                                                                                                                                                                                                                                                                                                                                                                                                        56 yTyrGluThrLysGluGluLeuIlePheArgTyrCysSerGlySerCysA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 ValLeuThrAlaIleHisLeuAsn....ValThrAspLeuGlyLeuGl
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ADDRESSEE:
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Ratio:
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: United States
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1840 DeHavilland Drive
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2.000
67.500
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Gaps: 1
Percent Identity: 30.000
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seq_documentation_block:
Sequence 1, Application US/08535682;
Patent No. 5731284
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY: inferred amino acid sequence for mature human GDNF US-08-564-833-1
                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/laa/5A_COMB.pep:US-08-535-682-1
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                                                                                                                                                                        APPLICANT: Williams, I
TITLE OF INVENTION: WE
TITLE OF INVENTION: US
TITLE OF INVENTION: F8
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 134 amino acid
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REFERENCE/DOCKET NUMBER: A -
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805.447-8102
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NAME: CUTTY, Daniel R.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 ATCTTGCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
COMPUTER_READABLE FORM
                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 ATGGTTCTCAGAACCATTTC 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 spAlaAlaGluThrThrTyr 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 yTyrGluThrLysGluGluLeuIlePheArgTyrCysSerGlySerCysA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
                                                              STATE: California
                                                                                   STREET: 1840 DeHavilland Drive CITY: Thousand Oaks
                                       COUNTRY:
                                                                                                                                 ADDRESSEE: AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 805-499-8011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
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                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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2.000
67.500

    Lawrence R.
Method for Treating Alzheimer's Disease
Using Glial Cell Line-Derived Neurotrophic
Factor (GDNF) Protein Product

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, NAME/KEY: inferred amino acid sequence for mature human GDNF US-08-535-682-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-446-383A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08446383A Patent No. 5733875
                              ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Ve

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Martin, David
TITLE OF INVENTION: METH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,682
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Curry, Daniel R.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 ATGGTTCTCAGAACCATTTC 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acid residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 ValLeuThrAlaIleHisLeuAsn.....ValThrAspLeuGlyLeuGl 56
                                                                                                                                                                                                                            STREET: 1840 DeHavilland Drive CITY: Thousand Oaks
                                                                                                                                                               COUNTRY: US
ZIP: 91320-1789
                                                                                                                                                                                                           STATE:
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APPLICATION NUMBER: US/08/446,383A FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                     ADDRESSEE: AMGEN INC
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2.000
67.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,727
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Gaps: 1
Percent Identity: 30.000
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                                                            Version #1.30
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seq_documentation_block:
   Sequence 1, Application US/08795628
   Patent No. 5736516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: Protein
; LOCATION: 1..134
; OTHER INFORMATION:
US-08-446-383A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-795-628-1
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US-09-030-606-115 x US-08-446-383A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Louis, Jean-Claude
APPLICANT: Louis, Jean-Claude
TITLE OF INVENTION: Methods for Treating Photoreceptors Using
TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor (GDNF) Protein
TITLE OF INVENTION: Product
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ATTORNEY/AGENT INFORMATION:
NAME: CUTTY, Daniel R.
REGISTRATION NUMBER: 32,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 ATCTTGCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGG 185
ATTORNEY/AGENT INFORMATION:
                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/564,833
                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 ATGGTTCTCAGAACCATTTC 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 yTyrGluThrLysGluGluLeuIlePheArgTyrCysSerGlySerCysA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 ValLeuThrAlaIleHisLeuAsn.....ValThrAspLeuGlyLeuGl 56
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                               STREET: 1840 DeHavilland Drive CITY: Thousand Oaks
STATE: California
                                                                                       APPLICATION NUMBER: US/08/795,628 FILING DATE: 06-FEB-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: AMGEN INC
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linear
                                                                                                                                                                                                                                                                                                                            United States of America
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2.000
67.500
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; NAME/KEY: inferred amino acid sequence for mature ; NAME/KEY: human GDNF US-08-795-628-1
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US-09-030-606-115 x US-08-795-628-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-519-777-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 76,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEEFREY D.
APPLICANT: KOTZBAUER, PAUL T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A --
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 TAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGG 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 ValLeuThrAlaIleHisLeuAsn.....ValThrAspLeuGlyLeuGl 56
                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                      CITY: ST. LOUIS
STATE: MISSOURI
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                                                                                                                                                                                                                                                                                                                ZIP: 63105-1817
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                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Ratio:
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5739307
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amino acid
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(314) 727-5188

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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-519-777-76
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   Quality:
US-08-618-543-1
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                                                                                  CURRENT AFFILIANTION NUMBER: US/08/6
APPLICATION NUMBER: US/08/6
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CULTY, Daniel R.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
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Percent Similarity:
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INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: USIN
TITLE OF INVENTION: USIN
TITLE OF INVENTION: PIOT
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quence 1, Application US/08618543
tent No. 5741778
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 ATCTTGCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Martin, David
APPLICANT: Miller, Gerald D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 ValLeuThrAlaIleHisLeuAsn.....ValThrAspLeuGlyLeuGl
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TYPE: amino acid
                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yTyrGluThrLysGluGluLeuIlePheArgTyrCysSerGlySerCysA 73
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                    TYPE:
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Using Glial Cell Line-Derived Neurotrophic Factor (GDNF)
Protein Product
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Percent Identity: 30.000
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; MOLECULE TYPE: protein US-08-742-035-76
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US-09-030-606-115 x US-08-618-543-1
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                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742/035
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/519,777
FILING DATE: 28-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 76, Application US/08742035 Patent No. 5747655
                                                                                                                                  TELEFAX: (314) 727-60 INFORMATION FOR SEQ ID NO:
                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acid
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 ATCTTGCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS NUMBER OF SEQUENCES: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 ATGGTTCTCAGAACCATTTC 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 yTyrGluThrLysGluGluLeuIlePheArgTyrCysSerGlySerCysA 73
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CITY: ST. LOUIS
STATE: MISSOURI
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ZIP: 63105-1817
                                              TOPOLOGY:
                                                                  TYPE: amino acid
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alignment_scores: Quality:

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Ratio:

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Length: 40
Gaps: 1
Percent Identity: 30.000

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366
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                  Query
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Copyright (c) 1993 - 1998 Compugen Ltd.
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  G37241
                                                 SUMMARIES
                  Description
 G37241 SHGC-57295
                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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DEFINITION
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G37241.1
                  Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157259687
                                                                                                       Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 374)
                                                                                                                                                                                     SHGC-57295 Human
G37241
                                                                            Human STSS (1997)
Unpublished (1997)
                                                                                                                                       Homo sapiens
                                                                                                                                               human
Email: myers@shgc.stanford.edu
                                                                                                Myers,
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7 ATF18F4
35 AC005444
37 AC005786
34 AC006786
34 AC006910
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D8709
6 CEKO8E3
1 AC006710
1 AC006710
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1 ACO06900

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CEY51A2D

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7 PCU43145
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1 ATACO06570
1 AC005919
6 CEC01G6
7 AF145052
                                                                                                                  Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
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L AC005696
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                                                                                                                                                                                                        DNA
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                                                                                                                                                                                             STS genomic, sequence tagged site.
                             CA 94305, USA
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AL021637 Arabidops
AC007180 Drosophil
AC005444 Drosophil
AC006786 Caenorhab
AC006790 Caenorhab
AC006910 Caenorhab
AC006910 Caenorhab
AF043701 Caenorhab
D87009 Human (lamb
D87009 Human (lamb
C81556 Caenorhabdi
AC006710 Caenorhab
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                                                                                                                                                                                                                                                                                  U43145 Plasmodium
AC005498 Homo sapi
AC006570 Arabidops
AC005919 Homo sapi
Z35595 Caenorhabdi
AF145052 Plasmodiu
166494 Sequence 14
D12772 Tetrahymena
AC006364 Homo sapi
AL022161 Human DNA
AC005402 Mus muscu
AC006624 Caenorhab
AC006785 Caenorhab
AC006900 Caenorhab
Continuation (3 of
AL021497 Caenorhab
CONTINUATION (3 of
AL021497 Caenorhab
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Result No.

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LOCUS
DEFINITION
ACCESSION
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KEYWORDS
SOURCE
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Best Local Similarity
Matches 291; Conserv
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                                                                                                                                                                                                                                                                                                                    135 CATCTTGCTTTTTCCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAAC 194
                                                                                                                                                                                                                                                                                                                                                      374 TATATTGTGTTGCAAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATC 315
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                                                                                                                                                                                                                CACCCAGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATA 314
                                                                                                                                                    ACAAACCCTGCTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTAGTC
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                                                             MMU88542
Mus musculus
U88542
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Primer B: TGCTTTTCCCCATTGGAAC
STS size: 200
PCR Profile:
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             house mouse.
  musculus
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AmpliTag Gold :
Total Vol:
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/db_xref="taxon:9606"
/map="8"
/clone_lib="Human"
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KC1:
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PCR Cycles:
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Pred. No. 6.1e-53;
0; Mismatches 0;
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project).
AL021637
g2827644
AL021637.1
                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 93646)
Bevan, M., Murphy.G., Drost,L., Hall,C., Hudson,S., Ridley,P., Bancroft,I., Mewes,H.W., Mayer,K. and Schueller,C.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
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Sciavolino, P.J., Abrams, E.W., Yang, L., Austenberg, L.P., Shen, M.M. and Abate-Shen, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 3145)
Sciavolino, P.J., Aus
Direct Submission
2 (bases 1 to 93646)
EU Arabidopsis sequencing, project
                                                                                                                                                            Arabidopsis thaliana
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/note="encodes the homeobox"
a 760 c 794 g 822 t
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/db_xref="G1:2105350"
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/db_xref="taxon:10090"
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thaliana DNA chromosome 4, BAC
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CBS	exon	gene	intron	exon	intron	exon	exon		CDS	gene	TITLE JOURNAL FEATURES source
complement()oin(43374424,44994645,47395174, 59456138,62836882,83918639,87429232)) /gene="F1884.20" /gene="f1884.20" /note="similarity to downy mildew resistance protein RPP5, Arabidops1s thaliana, parchx:G2109275" /codon_start=1 /product="downy mildew resistance-like protein" /protein_id="CAA16600.1" /protein_id="CAA16600.1" /db_xref="PID:g12877646" /db_xref="PID:g12877646" /db_xref="SPTREMBL:049419" /translation="MapAFRRPPRPQIYISFOGNDLRKGFVSHVVKALKDARVNVFVDN /translation="MapAFRRPPRPQIYISFOGNHQLTHIIVGCLRSIARKPSFTS GYYSNDSDLVEAIIGGIKKKIPYISAKQTIGEEVSAELLSASVVAALCEFFIPISVFP DLGFFISFRWYLAVMLFVVRHSLRSYQARRDPDSFPPPIPESRRPFDLFPFVLIF RPRPPLPYARPLOPPOSLPPRPRPQVFVSFRGKELRHGFVSHVVKALRIAGVNVFIDS NEMKGRDLQNLFKRIENSKMALVIFSDRFSESDWCLNELVKIDDCVKEGKLTVIPVFY	24)	complement(32193270) /gene="F18F4.10" /number=4 /10mber=4 43379232	/number=3 /number=3	/gene="F18F4.10" /gene="F18F4.10"	/gene="F18F4.10" /number=2 complement(4712693)	.0	SCLNECFRYINTGFATC KLETSDVRLLKQEFGTN complement(141. /genc="F1884.10" /number=1	/note="Protein sequence is in conflict with the conceptual translation." /codon_start=1 /product="hypothetical protein" /protein_id="CAA16599.1" /db_vref="PID:q2827645" /db_xref="PID:q2827645" /db_xref="SPTREMBL:049418" /translation="MAKILCSYLFICMEVLSGFLVFSSAKOLKTCTSVIKLGHPCDIE	/gene="F18F4.10" complement(join(138251,322470,26942855,32193270)) /gene="F18F4.10"	/organism="Arabicopsis thallana" /variety="Columbia" /db_xref="taxon:3702" /chromosome="4" 138. 3270	Direct Submission Submitted (03-FEB-1998) MIPS, at Blochemie, Am Klopferspitz 18a, Coordinator: Mike Bevan, Molecul Laboratory, John Innes Centre, C E-mail: michael bevan@bbsrc.ac.u Location/Qualifiers 1, 93646
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/db_xref="q" /db_xref="q" /db_xref="q" /db xref="q" /db xref="q" /translatic /translatic /translatic /translatic /translatic /translatic /translatic /translatic /translatic /fintTractiv /fintTractiv /fintTractiv /gene="fill /number=1 /fumber=1 /f	/codon_stan /product="p /protein_ic /db_xref="p	/gene="F18F 12070133 /gene="F18F /note="simi	12070133 /gene="F18F /number=1 12070133	/number=6 complement(/gene="F18I /number=7	/number=6 complement(/gene="F18E	/gene="F18E /number=5 complement(/gene="F18E	/number=4 complement(/gene="F18] /number=5 complement(/gene="F18E /number=3 /number=3 /omplement(/gene="F18E /number=3 complement(/gene="F18E /number=4 complement(/gene="F18F /number=2 complement(/number=1 complement(/gene="F18F /number=2 complement(RVNTDDVKNFF YLVDAIVRDVF WFVVFINHGES VIFSDRYTASS TIGGFRDHPFS RVQDEKLPSFI Complement /gene-"F188

FKGKFGSCFIETVQRQSPKEEPMAERWVNSVKSISSKTGFTSEVHRIDS
VKRQLPVVDTKEKELPIETEJLTFALVLAGLCHTAPLIENDTSFYKTPQ
ESDQSDGFIRHVERALNDEGFNVFIDSDERRGRGMEHIFRAIDNSNVAL
SELCLHEAVRIYDERREGKLVLIPVFYRVSEDDVMMFNGREGESFLETL
FALHWARNVNFICTDTGFTSADYSSNDTSLVEEIVRAIKRRLQGKKLPR
PLDMFMPKQPNAQEGLDVFSILQMLVAVLSLVVIRKTFRLILS"
L(4425. .4498)

t(4499. 8F4.20" .4645)

t(4739. 8F4.20" t(4646. 8F4.20" .4738) .5174)

t(6139. 8F4.20" t(5945. 8F4.20" t(5175. 8£4.20" .6138) .5944) .6282)

t(6883. 8F4.20 t(6283. 8F4.20" .8390) .6882)

t(8391. 8F4.20" .8639)

t(8742. 8F4.20" t(8640. 8F4.20" .9232) .8741)

3365 8F4.30"

"similarity to W20DMY30S"

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eff= 5942 8F4.40"

5942 8F4.40" 5942 8F4.40" nilarity to W15DMY30S"

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Eukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 119707) 1 (bases 1 to 119707) 2 (bases 1 to 119707) 3 (bases 1 to 129707) 4 (bases 1 to 129707) 5 (bew.m., Chev.S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Rutenhoff, C., Champe, M., Chavez, C., Chew.M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
                                                                                                                                                                                                                                                                                                                                                                                          unordered pieces.
AC007180
g4827280
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ONVVLAVFSLVVIFVLFLVVHVYMTALMHLASVVSVLEPIYGLAAMKKSYELLKGKTL
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LQVPGDIFWKYNGLLEYGGKIAILNYTKVDIEGVMELMVVEDEEKNLWSSKILVVNPL
QLQMVNSIISLTVLGTTRNGEVILVPGPEDKTVFNILLYDLQKNHIRKIEIKGGPDRY
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DKSALHDHLGGYLGEVYPLKSNIQMENFEV"
18489. .19371
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Celniker, S.E., Agbayan, A., Arcaina, T.T., Baxter, E., Blazet, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R. A., Harris, N. L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney Kin, E., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Poon, L., Sequelta, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. (Buth, C.M.)
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Direct Submission
Submitted (29-MAR-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On May 14, 1999 this sequence version replaced gi:4764154.
Por further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruiffly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 400 bases, phrap computed error

Sg

NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. as soon as it is available and the accession number will be preserved. contig of 1042 bp in gap of unknown lengt contig of 725 bp in of 1042 bp in length length length

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                                            Celniker, S.E., Georgé, R.A., Galle, R., Svirskas, R.R., Hoskins, R.A., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zharan, L.L., and Kimmel, B.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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AC005444.1 GI:3818341
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Sequencing of Drosophila chromosome 2R, region 36D3-36D3
Unpublished (1998)
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1 (bases 1 to 77685)
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/strain="y2; cn bw sp"
/db_xref="taxon:7227"
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Pl library location: 67-43.
* arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number wil
* be preserved.
                                                                                                         Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Mar 1, 1999 this sequence version replaced gi:4263152.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                    Direct Submission
Submitted (23-FEB-1999)
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Waterston, R.H.
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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Caenorhabditis elegans clone Y48G8, WORKING DRAFT SEQUENCE, 13
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/clone_lib="P1 library, part
/clone="P1 DS06379 (D358)"
16311 c 15292 g 22141 t
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/db_xref="taxon:7227"
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                                                    AC006798.2 GI:4309785
HTG: HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 207370)
Waterston,R.H.
 The sequence of Caehorhabditis elegans clone Unpublished .2 (bases 1 to 207370)
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/db_xref="taxon:6239"
/clbone="Y4868"
/clbone="Y4868"
46255 c 46078 g 84102 t 2411
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202845: contig of 35708 bp in length
202845: contig of 35708 bp in length
202846: contig of 2230 bp in length
205084: contig of 2230 bp in length
205093: gap of unknown length
209517: contig of 4424 bp in length
209526: gap of unknown length
221793: contig of 12267 bp in length
221802: gap of unknown length
221802: gap of unknown length
228079: contig of 6277 bp in length
231641: contig of 3553 bp in length
231641: gap of unknown length
231649: gap of unknown length
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81454: contig of 65419 bp in length
8163: gap of unknown length
161281: contig of 79818 bp in length
161290: gap of unknown length
163945: contig of 2655 bp in length
163945: gap of unknown length
167128: contig of 3174 bp in length
167127: gap of unknown length
167137: gap of unknown length
202845: contig of 35708 bp in length
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Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Lou Mo 63108, USA
On Mar 1, 1999 this sequence version replaced g1:4263140.
* NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                MO 63108, USA
On Mar 1, 1999 this sequence version replaced gi:4263438.
NOTE: This is a 'working draft' sequence. It currently
consists of 36 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                     unordered
AC006910
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Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
Eukaryota; Mehabditodea; Rhabditina; Rhabditodea; Rhab
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Caenorhabditis elegan
                                                                                                                                                                                                                  Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                         Direct Submission
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Waterston, R.H.
                                                                                                                                                                                                                                                                     Unpublished
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/db_xref="taxon:6239"
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Matches 98;

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 40479)
Wamsley, P. and Kramer, J.
The sequence of C. elegans c
Unpublished (1908)
3 (bases 1 to 40479)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Laister, N., Laister, N., Januare, B., O'Callaghan, M., Farsons, J., Percy, C., Hifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vandhan, M., Santhan, M.,
                                                                                                                                                                                                                                               Submitted (20-JAN-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Caenorhabditis elegans
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AF043701
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(bases 1 to 40479)
Wilson, R., Alnscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
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                                          Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England
                                                                                                                       Department of Genetics, Washingst. Louis, MO 63110, USA, and
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                             Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:2804466
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                                                                                                                                                                  Washington University
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NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION

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The 5' cosmid is Y48G8A;3' cosmid is GAPlarm_65, 200 bp overlap. Actual start of this cosmid is at base position 1 of CELK12C11; actual end is at 40479 of CELK12C11
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NOTES:

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains similarity to ubiquitin-like proteins; coded for by C. elegans cDNA yk118b3.3; coded for by C. elegans cDNA yk62e7.3; coded for by C. elegans cDNA yk74b5.3; coded for by C. elegans cDNA yk14h3.3; coded for by C. elegans cDNA yk114h3.3; coded for by C. elegans cDNA yk118b3.5; coded for by C. elegans cDNA yk118b3.5; coded for by C. elegans cDNA yk118b3.5; coded for by C. elegans cDNA yk112e2.5; coded for by C. elegans cDNA yk114h3.5; coded for by C. elegans cDNA yk12e2.5; coded for by C. elegans cDNA yk114h3.5; coded for by C. elegans cDNA yk138b5.5; coded for by C. elegans cDNA CEESY60RB; coded for by C. elegans cDNA yk138b6.5
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ITIEPGCYFIDFLANEALADFKKSEFLVKSEIDKYRGSGGVRIEDDVIIRASGNENLS
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complement (1200. 1581)
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QAMYHEWQTLLAFILMNIYMTENKKMKISGPPEMHMWFHTKTQDTVLFKTWNVTDTPT
MVWVCCIIVVAGILLELIKFLRWKIEKWHKNRDELVSRSYISRLFSPIHIGQTILFMV
QLSFSYILMLLFMTFSVWLGIAVVVGLGIAMMMDMMQMYFHFRIQEPILFRQWKPTDT
                                                                                                                                                                                                                                                                                                                         complement(join(2574. .2653,2665. .2720,2914. .3008, 3289. .3479,4202. .4347,4912. .5029,5168. .5270,5985. 6126. .6288,6769. .6889))
                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2574. .6889)
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adrtgvavnslrelfdgrrindddtpktlemedddvievyqeqlggf"
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/db_xref="PID:g2804467"
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                                                                                                                                                                                       /evidence=not_experimental
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/gene="K12C11.1"
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/chromosome="I"
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Similarity 50.5%;
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FGLSREIEPGAVVKDWGTPEEVAPEVVNYEALSPATDMWAVGVVTY ILLSGGSPELG
FGLSREIEPGAVVKDWGTPEEVAPEVVNYEALSPATDMWAVGVVTY ILLSGGSPELG
DNDETF SNITRVYHSDRYFKNTSKHAKDET IY KLFVBOVDQRATVEECLQHPWIRG
DNRDETF SNITRVYHSDRYFKNTSKHAKDET IY KLFVBOVDQRATVEECLQHPWIRG
PEGNALDIKRASCITISHIQSEKTRQRKKKCVELVWYLLKASKSSFRIGOGREDEDM
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VFNYEHMKGGNICARDNGDTPLHVACREAQHTVAGYVANEKIDVDSINKTGETALHC
AVENDTRVYELLLQARPRLDLPNAREETPLHVAAARGHVDCVQALLDANSPIDAVEQ
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ARGBSESATSMFYFMEDLINLVEHAAAEVGFGISLERHFISPHHERHPALFPPE
FROMMENDORESISVENGTONEFEFTNVCGFGSDDVABUTTGINVGADNOMASGFIA
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(lambda) DNA for
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CLLDEPHAMGRDWSILAVKLQLTDQVEDVDSTGQSLSRTDQLLNEWALHHPEQASVGN
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25918. .26212
/note="C. elegans telomere-like hexamer repeat"
1 7528 c 7289 g 12244 t
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KKRRYATSRRGVTRQNIEREVRYLQKIRGNSNYVELHAVYETASDVIIVLELVSGGEL
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complement(join(4133..14396,15675..16211,17274..7854..1905,19953..20502,21661..21936,22047...2

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Pred. No. 2.8;
                                                                        immunogloblin light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawasaki,K., Minoshima,S., Nakato,E., Schmeits,J.L., Wang,J. and Shimizu,N. One-megabase sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 104386)
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complement(68859. .70486)
/gene="5"0Y11.1"
complement(68859. .>70486)
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7092. .7382
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/gene-"5'0111
                                                                                                                                                 /gene="V3-1P"
                                                                                                                                                                                                                                               PKLLIYYDDLLPSGVSDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="QPVLTQPPSSSASPGESARLTCTLPSDINVGSYNIYWYQQKPGS"
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'gene="V4-1"
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Best Local Similarity
Matches 71; Conserve
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281568.1
                                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
(bases 1 to 39565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
281568
Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail:
                                                                                                 McMurray,A.
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EYYGGDHGGDGOEOKTHTTFKCLSCVKVLKNIKFMHMKHHLEFKORNDSWEDHTTC
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VCQVCHYRSSVFADVETHFRTCHENTKNLLCLFCLKLFKTAIPYMNHCWRHSRRRVLQ
CSKCRLQFLTLKEEIEHKTKDHQTFKKPEQLQGFPRETKVIIQTSVQPGSSGMASVIV
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ENPIVLLSDFYYGQHKGEGQPEQKTHTTFKCLSCVKVLKNVKENHVKHHLEFEKQRN
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HHKPGEMPYVCQVCHYRSSVFADVETHFRTCHENTKNLLCPFCLKIFKTATPYMCHYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small coverlap between neighbouring submissions.

This sequence is the entire insert of clone KOBE3. The true right end of clone WOGF12 is at 467 in this sequence. The start of this sequence (1. 105) overlaps with the end of sequence ZB3244.

The end of this sequence (39514. 39565) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jes@sanger.ac.uk or rw@nematode.wustl.edu

2 (bases 1 to 39565)

8 (Milson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Coulson,A., Gracton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Coulson,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latretille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
C'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Therry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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On Sep 23, 1998 this sequence version replaced gi:3294143.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
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2 (bases 1 +^ ''
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Current sequence finishing criteria for the C. elegans genome
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                                                                                                               /translation="mrwipilitilllcvvlisvagvkstikkgavggtavrktivkk
vavenkniqrungkrwrepprocsdapkhlkqtclmirrmdlatrrrlargsvrqtrp
nqvpnwlqpippanargqaaxhpydcmtllclcpfergrnvngcvlsngvvlnmsw
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krvelalrwydptveippwdsvmdsvlpdprosimfsdlfvggtdygnvtgpfayw
rtiegrstilrnlgaegqlfnenqvntivaqntientlaytapdpggpypnnygaiey
shshihlwiggdmkppstsanepiffmhhsfydylwelwrolodprwlredaysadhp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"similar to Common central domain of tyrosinase; CDNA EST EMBL:214371 comes from this gene; CDNA EST CEMSG81F comes from this gene; CDNA EST EMBL:M89185 comes from this gene; CDNA EST EMBL:C13572 comes from this gene; CDNA EST EMBL:C13572 comes from this gene; CDNA EST yk240a11.3 comes from this gene; CDNA EST yk240a11.5 comes from this gene;
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4998. .5101,5288. .5683,5730. .6167,6215. .6358)
/gene="K08E3,1"
TCANWQHFSYAPMRPFPYLVNRDGLSNSYTDQMYRYAPRATCSHQRPNCGSPYLFCDT
RGYPHCVSKIRLNGNCRGFEQNDACYASRCWWGRCVNANFAARWKGARTHANSTLIDL
ELAKEVSVNGTKVERVPLVKRISIKWTAPLFVDCYNRWPCCDSWAKNGGCQREPEFMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3510. .6358
/gene="K08E3.1"
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/chromosome="III"
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/db_xref="pid::e1347998"
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/db_xref="pid::e1878437"
/db_xref="gi::3878437"
/db_xref="gi::3878477"
/db_xref="gi::3878477"
/db_xref="gi::3878477"
/db_xref="gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"predicted using Genefinder; similar to EF hand, Src homology domain 3; cDNA EST EMBL:D64948 comes from this gene; cDNA EST EMBL:D65652 comes from this gene; cDNA EST EMBL:D60652 comes from this gene; cDNA EST EMBL:D70789 comes from this gene; cDNA EST EMBL:C13458 comes from this gene; cDNA EST EMBL:C13458 comes from this gene; cDNA EST EMBL:C3458 comes from this gene."
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16055. .16259,16305. .16386,16433. .16509,16656. .16905,
17201. .17392,17487. .17593,17642. .17692,18137. .18266,
18350. .18524,18574. .18631)
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TTRSMSCSTNOSSSKTIEDVLSGEAGNSSSADDSSKNILTQLETTPKKLISSPKTSK
SSTPTDLRRABISSPKLIKRSEFSGALIRKSLETPDSVKVETAVTVTALFEFAKSSAET
MSIEQGEILLVLEHDHGDGWTRTKNCRKHNEESGFVPTSYLQFPO*
101n(14167...14295,14596...14763,14810...14911,15156...153)
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complement(join(6755. .6953,7015. .7141,7190. .7388,
7618. .7680,7727. .7969))
/gene_"K08E3.2"
/note_"predicted using Genefinder"
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15357. .15472,15522. .15645,15694. .15854,15902. .16007,
16055. .16259,16305. .16386,16433. .16509,16656. .16905,
17201. .17352,17487. .17593,17642. .17692,18137. .18266,
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14167. .18631
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yk273e3.3 comes from this gene"
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CONTROL OF COMES FROM EST WALLDY SET WALLDY SET WALLDY SET EMBL: X14844 COMES FROM This gene; CDNA EST EMBL: X14802 COMES FROM THIS gene; CDNA EST EMBL: X14502 COMES FROM THIS GENE; CDNA EST YX20748. SCOMES FROM THIS GENE; CDNA EST YX20748. SCOMES FROM THIS GENE; CDNA EST YX20749. SCOMES FROM THIS GENE; CDNA EST YX20741. SCOMES FROM THIS GENE; CDNA EST YX328411. SCOMES FROM THIS GENE; CDNA EST YX328411. SCOMES FROM THIS GENE; CDNA EST YX3555. SCOMES FROM THIS GENE; CDNA EST YX35594.4 SCOMES FROM THIS GENE; CDNA EST YX3594.5 COMES FROM THIS GENE; CDNA EST YX3994.5 COMES FROM THIS GENE; CDNA EST YX3994.5 COMES FROM THIS GENE; CDNA EST YX4994.5 COMES FROM THIS GENE; CDNA EST YX4954.5 COMES FROM THIS GENE; CDNA EST XX465412.3 COMES FROM THIS GENE; CDNA EST XX465412.3 COMES FROM THIS GENE; CDNA EST XX465412.3 
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EATIEQPAPFELEDLGDPKNCDSRTNDSADGSGKLLKSSPSKNRI IRNELGILKEKE
ADEKPEASNNUDCHMYTDNSKPAHVLLSCLRSK IRDMEKOLEQATOGREGITRLOQAYY
TNOQHONPSACTEPLI SYAKKI EKLKHDI HNLKEFYAHLEMSVEEGQERSFGGRDTPD
TTRSMSCST NOSSK I I EDVLGGEAGNSSADDSKNI L I KOLFT T PKRLI SSPKTSK
SSTPFLRRAEI SSPKI LRSEFSGA I KKSLSTPDSVKVETAVTVTALFEFAKSSAET
MSI EQGEILL VLEHDHGDGWTRTKKKHNEESGFVPTSYLOFPO"
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20433. .20734,21052. .2
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/codon_start=1
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.21164,21214. .21352))
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Query Match Best Local Matches 93; Similarity Conservative /protein_id="CAB04592.1" /db_xref="PID:e1347999" 10.8%; 51.1%; 0 Score 39.6; DB Pred. No. 4.2; Mismatches 36; ; 68 Length 39565; Indels 0 Gaps 0

SOURCE ORGANISM VERSION KEYWORDS ACCESSION DEFINITION g4263228 AC006710.1 GI:4263228 HTG; HTGS_PHASE1. Caenorhabditis elegans. Caenorhabditis elegans unordered AC006710 AC006710 145920 bp DNA HTG 23-FEB-1999 Caenorhabditis elegans clone Y119C1AA, WORKING DRAFT SEQUENCE, pieces.

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 129638 CAATTTTCTAAAGTCGAATTTTTTTGTTTGTAGAAAATAAGTTACTTTTATAAGAGAATTG 129697
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                                                           Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; S:
Rhabditina; Rhabditoidea; Rhabd
1 (bases 1 to 299919)
Waterston, R.H.
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Unpublished
                                                                                                                                                                                                                                                                                            AC006712 299919 bp DNA HTG 23-FEB-1999 Caenorhabditis elegans clone Y119Clb, WORKING DRAFT SEQUENCE,
                                       The sequence of Caehorhabditis elegans clone
                                                                                                                                                                                   AC006712.1 GI:4263226
HTG: HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence of Caehorhabditis elegans
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Waterston, R.H.
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Waterston, R.H.
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/db_xref="taxon:6239"
/clone="Y119C1AA"
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Pred. No. 5;
0; Mismatches 137;
                                                                                                  oda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis
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Best Local Similarity
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TITLE
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                                                                                                                                                                                                                                         Fragment Name CEY111B2_0 CEY111B2_1 CEY111B2_2 CEY111B2_3 CEY111B2_3
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CEY111B2_5
CEY111B2_6
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Z98857.32
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhab
                                                                                                                                      Caenorhabditis elegans DRAFT SEQUENCE, in unor
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Direct Submission
Submitted (23-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                     HTG; HTGS_PHASE1
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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/db_xref="taxon:6239"
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Mismatches 137;
 oda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditi
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Matches 88; Conserv
                                                                                                                                                         Query Match 10.6%;
Best Local Similarity 51.8%;
Matches 88; Conservative
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CEV111B2_1
CEV111B2_2
CEV111B2_3
CEV111B2_4
CEV111B2_6
CEV111B2_6
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                      83 TGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGC 142
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                                                                                                 AATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTG 82
TTTGGCGGGAATTCAAATTTTAATTTTTTGAAAATATTTTGGCGGGAATTCAAAATTTA 6078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29 MAY-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jcs@sanger.ac.uk or rw@nematode.wustl.edu on Jun 1, 1999 this sequence version replaced gi:4877274.
Order of segments is not known; 800 n's separate segments.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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1. .613487
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/db_xref="taxon:6239"
/chromosome="unknown"
/clone="Y111B2"
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Search completed: September 28, 1999, 12:23:29 Job time: 5089 sec

29.8 29.6

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Polynucleotide seq Human secreted pro

ALIGNMENTS

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run 9: September 28, 1999, 12:27:16; 16 ; Search time 289.74 Seconds
(without alignments)
316.043 Million cell updates/sec

Title: Perfect score: Sequence: US-09-030-606-115
366
1 GCTCTTTCTCTCCCCTCCTC.....CTGTGACTTGAAGTTTAGTC 366

Searched: Scoring table: IDENTITY_NUC 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 4444 80 444 80 80	00 00 00 00 333 334 340	0 00000 0 0000 1222 1235 1286	0 000000000000000000000000000000000000	Result
30.2 30.2 30.2 30.2 30.8				
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QY 1 GCTCTTTCTCCCCCCCCCCTCGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60	Query Match 100.0%; Score 366; DB 1; Length 366; Best Local Similarity 100.0%; Pred. No. 9.2e-90; Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC cancers. SQ Sequence 366 BP; 102 A; 78 C; 58 G; 128 T;	 CC encoded by this sequence). An antibody which binds to an immunogenic CC portion of the prostate protein, and the method can be used to detect,	able to		for detecting and treating prostate cancers		PT Dillon DC. Xu. J:	PR 01-AUG-1997; US-904809.	09-FEB-1998;	PF 25-FEB-1998; U03690.		OS Homo sablens	Prostate	Prostate tumour specific gene clone.	08-DEC-1998 (first entry)	V58588;	ID V58588 standard; cDNA; 366 BP.	V58588	RESULT 1	

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pi Dillon DC, Xu J;
DR WPI; 98-609886/51.

PT Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
PS Claim 3; Page 85; 130pp; English.

CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted CDNA library obtained by
CC subtracting a prostate tumour CDNA expression library with a normal
CC tissue cDNA library.

SO Sequence 366 BP; 102 A; 78 C; 58 G; 128 T;
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W09837093-A2.
27-AUG-1998.
25-FEB-1998; U03492.
09-FEB-1998; US-806099.
01-AUG-1997; US-806099.
01-AUG-1997; US-908044.
Homo sapiens.
WO9837418-A2.
27-AUG-1998.
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Matches 265; Conserv
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09-FEB-1998; US-904809.

25-FEB-1997; US-904809.

01-AUG-1997; US-904809.

(CORI-) CORIA CORP.

Dillon DC, Xu J;

WPI; 98-480805/41.
                                                                                                                                                                                                                                                                                                                   Homo sapiens.

WO9837093-A2.

27-AUG-1998; UC

25-FEB-1998; UC

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This sequence represents a human prostate tumour specific gene, and car be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
                                              Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 94; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself. can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted CDNA library obtained by the process of the control of the treatment of prostate cancer.
                                                                                                                                                                                                                                            (CORI-) CORIXA CORI
Dillon DC, Xu J;
WPI; 98-609886/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-1999 (first entry)
cDNA sequence of prostate tumour clone.
Prostate; cancer; tumour; vaccine; immunogen; clone;
     subtracting a prostate tumour cDNA expression tissue cDNA library.
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Best Local Similarity

Matches 265; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus contig SEQ ID #98.

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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PS Claim 1; Page 584-590; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as priners or probes for isolating community readable medium.
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Matches 74
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(HUMA-) HUMAN GENOME SCI IN
Barash SC, Choi GH, Dillon
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16-MAY-1992
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07-JAN-1997; 100117
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making. The control of gene e
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31-JAN-1990.
20-JUL-1989; 810555.
29-JUL-1988; US-353312.
(CIBA) Ciba Geigy AG.
Shinshi H, Wenzler H, Hofsteenge J.
WPI; 90-031717/05.
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06-FEB-1992.
24-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant protein with endo chitinase activity - also DNA encoding it and plants which express it, resistant to fungi, insects, bacteria and nematodes.

Example: Fig 2; 82pp; French.

The inventors claim a new recombinant gene which codes for a protein with encochitinase activity, or its precursor (see 021007). The coding part of the gene contains at least the 5' part of DNA for tomato endochitinase and at least the 3' part of DNA for the tobacco enzyme (DNA can be genomic or cDNA, but at least one intron is pref. present). The recombinant gene includes the 35 promoter of cauliflower mosaic virus plus the terminator from the nopaline synthase gene of Agrobacterium tumefaciens.

Sequence 3012 BP; 965 A; 634 C; 436 G; 977 T;
                                                 Disclosure: Fig 8; 41pp; English.
Beta-1,3-glucanase is involved in plant de
it hydrolyses polyssaccharides, useful in
making. The clones allow for transfer of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q03253 standard; DNA; 4483
Q03253;
                                                                                                                                                                                 Recombinant DNA encoding be useful in plant protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-1,3-glucanase; papermaking; polysaccharide hydrolase
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(SNFI ) SANOFI SA.
(ERAP) SOC NAT ELF AQUITAINE.
Dubois M, Grison R, Leguay JJ, Pignard A,
                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUL-1990
                                                                                                                                                          from tobacco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry) clone pBSGluc39.1 encoding beta-1,3-glucanase
       expression.
BP; 1418
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                                                    defence against pathogens and in biomass conversion or paper f the gene to other species and
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Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
                   25-FEB-1999 (first entry)
Tobacco basic beta-1,3-glucanase genomic DNA clone pBS-Gluc39.1.
Regulation; transcription; plant tissue; chimeric construction; pathogenesis-related protein; anti-pathogenic; transgenic plant; beta-1,3-glucanase activity; pest resistance; ss.
                                                                                                                                                            4361
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                                                                                                                                                                                                                                                                                                                                                                                                       Claim 79; page 72-74; 117pp; English.
Sequence is a chemically inducible gene used to regulate transcription of an associated DNA sequence in plant
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 79; page 72-74; 117pp; Sequence is a chemically indu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                wpi; 89-265342/37.
Chemical induction of cloned genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ryals J, Montoya A,
Payne G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-5EP-1303-3

36-MAR-1989; 103888.

08-MAR-1988; US-165667.

(CIBA) Ciba Geigy AG.

(CIBA) Montoya A, Harms C,
Nicotiana sp. US5847258-A.
                                                                                   V72993 standard;
V72993;
                                                                                                                                                                                                                                                                                                                                                                      See also N90368, N
Sequence 4483 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         and processes for inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana tabaccum cv.
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Tobacco basic beta-1,3
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                                                                                                                                                                                   121
                                                                                                                                                                                                                                  61
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75; Conserv
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75; Consert
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                                                                                              cDNA;
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P; 1418 A; 837 C; 745 G; :
                                                                                                                                                                                                                                                                                                                     9.2%;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence and
to herbicide and
                                                                                                                                                                                                                                                                                                                                 Length 4483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding pathogenesis-related glucanase proteins - useful for producing transgenic plants with enhanced disease or pest resistance Example 3; Column 163-168; 169pp; English.

The present invention describes a DNA molecule encoding a pathogenesis-related (PR) protein having beta-1,3-glucanase activity selected from PR-2, PR-2', PR-N, PR-O', Also described are: (1) a chimeric gene comprising the above DNA molecule linked to a heterologous promoter; (11) a vector containing the chimeric gene; (11) a host cell containing the chimeric gene; (11) a transgenic plant containing the chimeric gene; (10) a transgenic plant. The DNA molecule is used to produce transgenic plants with enhanced disease or pest resistance. The present sequence represents a tobacco basic beta-1,3-glucanase genomic DNA sequence.

So Sequence 4483 BP; 1418 A; 838 C; 744 G; 1483 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 75
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31-MAY-1995; 457364.
31-MAY-1995; US-457364.
31-MAY-1995; US-165667.
08-MAR-1998; US-305566.
24-MAR-1989; US-305566.
24-MAR-1989; US-368672.
20-CUN-1989; US-36872.
20-CCT-1989; US-678378.
21-DEC-1990; US-678378.
21-DEC-1990; US-678378.
27-SEE-1991; US-678378.
27-SEE-1991; US-678378.
27-SEE-1991; US-973197.
06-MAR-1992; US-948506.
06-NOV-1992; US-973197.
16-APR-1993; US-045957.
16-JUL-1993; US-045957.
18-MAY-1994; US-181271.
(NOVS ) NOVARTIS ETIANCE CORP.
MOYET MB, Payne GB, Ryals JA, Wa
                                                                                                US5851766-A.
22-DEC-1998.
31-MAY-1995; 456262.
31-MAY-1995; US-456262.
(NOVS ) NOVARTIS FINANCE CORP.
HARTHS C. RYALS JA;
WPI; 99-080396/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4481
                                                                                                                                                                                                                                                                                                                                                                               Tobacco beta-1,3-glucanase gene clone pRSGluc39.1. Chemically regulatable DNA promoter; expression control; pesticide;
Isolating chemically regulatable DNA sequences in plants - for chemically controlling expression in transformed plants Example 33; Column 169-174; 175pp; English.
                                                                                                                                                                                                                                                                                                                              Nicotiana acuminata
                                                                                                                                                                                                                                                                                                                                                           herbicide tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V62789 standard; cDNA; 4483
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mes 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGTTTGTTGTGGCATGCTTCTT 4338
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; Pred. No. 3.4;
0; Mismatches
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CC fragment from the 5' flanking region of a chemically regulatable DNA promoter CC a plant tissue. The method allows isolation of sequences which will be CC useful for the controlled expression of genes, under the control of a CC non-coding regulatable sequence. This is useful in plants with a CC chemical regulator, the regulator being applied before or with the CC chemical regulator, the regulator being applied before or with the CC chemical regulator being applied before or with the CC is useful for controlling sequences which encode traits such as CC height, shape, development, male or female sterility, and the ability CC of the plant to withstand cold, heat, salt and drought. The chemical induction of the promoter allows the regulation of production of compounds, e.g. flavours, fragrances, pigments, natural sweeteners, CC industrial feedstocks, antimicrobials and pharmaceuticals, by CC biosynthesis or metabolite conversion, whose biosynthesis is controlled by endogenous or foreign genes. The method allows control over the time CC and rate of gene expression either throughout the whole plant, or in CC instance dusting the leaves with the chemical regulator. Controlling the developmental processes by the application of a regulating chemical in CC a given time. Flower formation and fruit ripening to be synchronised at a given time.
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V74317/c
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Best Local S
Matches 75
EP-786519-A2.
30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus contig SEQ ID #6.
Computer readable medium; vaccine; S.aureus infection; immunodet cellulitis; eyalid infection; food poisoning; osteomyelitis; the skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4361
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                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxic shock syndrome; ds.
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given in the specification for this DNA sec
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Pred. No. 3.4;
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Continuation (9 of 10) c
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Sequence 3601 BP; 1170 A; 496 C; 738 G; 1057 T;
                                                                                        Query Match
Best Local Similarity
Matches 67; Conserv
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MAGE-B cluster DNA; testicular seminoma;
carcinoma; ss.
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7961.
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23546.
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10 fragments
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103118 AAGTATTTCTACAATGTTTCAAAATATTATTCAAGATTTCAAATGCCGGAACATCGCTAA 103059
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X20248 Accession X20248
DB 1;
Length 10715;
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restriction and other properties. The invention and other cancers - using MAGE-R cluster DNA sequence. The invention provides a novel method for screening for the possibility of a testicular seminoma, concernmental in a sample. The method comprises contacting the sample with the at least one nucleic acid molecule which hybridises to mRNA corresponding to an MAGE-Xp gene, and determining hybridisation as a determination of comprises contacting the sample with method comprises contacting the sample with contained maker and control of the sample with hybridises to mRNA corresponding to an MAGE-Xp gene, and determining hybridisation as a determination of comprises contained which hybridises to mRNA corresponding to an MAGE-Xp gene, and determining hybridisation as a determination of melanoma, breast cancer, sarcoma, or leukaemia in the sample. By assaying for the MAGE-B1 gene, or MAGE-B gene, both contained within this 40352 completed that encodes the presence of such cancers in a sample can be determined. The genomic DNA that encodes the MAGE-B2 gene consists of nucleotides 3266-7979 of this MAGE-B cluster DNA sequence. The nucleic acid molecule that encodes a MAGE-B1 gene, consists of, in CC 5' to 3' order, nucleotides 31403-31474, 33958-34062, and 38088-39691, and mucleotides 335057-35139 and 38088-39691, and nucleotides 3358-34062 and 38088-39691 of this sequence. The primers specific for the MAGE-B cc gene can be used in a kit to amplify a MAGE-B gene.
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11-DEC-1997.
05-JUN-1997; U09774.
25-APR-1997; US-846111.
05-JUN-1996; US-658578.
(LUDM-) LUDWIG INST CANCER RES.
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                                                                                                                                                                                                                                                                                                      New yeast of controlled activation at low temperatures - useful for improving the quality of dough claim 5; Page 21-22; 41pp; Japanese.

The present sequence represents a protein phosphatase gene sequence of Saccharomyces cerevisiae. The specification describes new secrevisiae in which the growth and/or the fermentation activity is controlled at least in the range of 0-20 degrees Celsius. These yeast are prepared by deleting the function of at least one protein phosphatase gene. The yeast is useful in the production of dough. Sequence 1407 BP; 434 A; 222 C; 325 G; 426 T;
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Protein phosphatase gene; growth; 
dough production; yeast; ds. 
Saccharomyces cerevisiae. 
J11042090-A.
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X15658;
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(SHOS ) SHOWA SANGYO CO
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                                                                                                                                  TGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTT 140
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                           AGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGA 236
                                                       AGTGTTCGCAATAACCACCAAAAAATTACAAGACCGCTTGAATCGTAGTAAAGATAATGA 1070
                                                                                 GCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA
                                                                                                               TTTTGTCCAAAGAAGGAAAAGTATTTTGATTTCCATGATTTTTCGGATGATGATAACGA 1010
                                                                                                                                                                          TGAATCTGAGTCACAATGGTTTGAGCGTATGAGATCAAAAAATTACAATATCCAAACGTC
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STRANDEDDESS: single
TOPOLOGY: linear
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; TELEEAX: (703)836-9300
; TELEX: 899149
: INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base ----
TYPE:
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FO
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 0 0 0 0 0 0 0
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Best Local (
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FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6

FILING DATE: 26-AUG-1991

ATTORNEY/ACENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 10FORMATION:

TELEPHONE: (703)836-9300

TELEPHONE: (703)836-9300
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPOSIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STREET: 18
                         FILING DATE:
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1800 Diagonal Road,
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Conservative 19
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US-08-327-994A-3

US-08-425-061-1

US-08-425-061-3

US-08-425-061-4

US-08-425-061-5

PCT-US95-10203-21
                                                                                                                                                                    ; Score 36.6; DB
Pred. No. 0.19;
190; Mismatches
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Sequence 5, App...
Sequence 5, App...
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APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recomb
TITLE OF INVENTION: having
NUMBER OF SEQUENCES: 15
                                                                                                                                                   NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-JUN-1995
                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3012 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FR 90 09460 FILING DATE: 24-JUL-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 16:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 21-JUI
                                                                                                                                                                                                                                                  NAME: BENT, Stephen A REGISTRATION NUMBER:
                                                                               STRANDEDNESS:
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T: 3000 K Street, N.W.,
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20007-5109
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   intron
2384..2462
                                                                                                                                                                                                                                                                                                                                            UMBER: WO PCT/FR91/00607
21-JUL-1991
                                                  DNA (genomic)
                                                                                   single
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US-08-181-271A-5/c
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Best Local Similarity
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FEATURE:
NAME/KEY: intron
LOCATION: 2617..269
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME/KEY:
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                                                                                                                               NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
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                                                                                                                                                               APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
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                                               COUNTRY:
                                                                                                ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
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                                     10532
                                                                                   Hawthorne
                                                                   New York
                                                    USA
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                                                                                                                                                                                                               Ward, Eric R.
                                                                                                                                                                                                                                             Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                              Alexander, Danny C. Beck, James J.
                                                                                                                                                                                                                                                                               Neuhaus, Jean-Marc
Payne, George B
                                                                                                                                                                                                                                                                                                                 Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                               Meins, Jr., Fre
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                               Harms, Christian
                                                                                                                                                                                                                                                                                                                                                                                 Goodman,
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join(2167..2383, 2463..2616, 2698..3007,
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1942..2166
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                                                                                          Query Match
Best Local (
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ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION UNBER: 36,129
REFERENCE/DOCKET NUMBER: S-19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/678,378
FILING DATE: 1 -APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
4481 GCTCTTTTGCTGCTCTGAATAGAGTCTTCTTTCCTGCCTTTGGAGTTGATGAAATGGA 4422
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 4483 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 27-SEP-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/632,441 FILING DATE: 21-DEC-1990 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/165,667
FILING DATE: 8 MAR-1988
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US (FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/093,301 FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                   1 GCTCTTTCTCTCCCCCTCCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
                                                                              1 Similarity
75; Conserv
                                                                                                                                                                                                                                                                           4483 base pairs
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ER: S-19825/P1/CGC 1727
                                                                        ; Score 33.6; D); Pred. No. 1.1; O; Mismatches
                                                                                                                 DB 1; Length 4483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                    APPLICATION NUMBER: US 07/165,667 FILING DATE: 8-MAR-1988 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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APPLICANT
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION UMBER: US 07/305,566
FILING DATE: 6-FEB-1989
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WIIIIAMS, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DAA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/449,315 FILING DATE: 24-MAY-1995
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CITY: Hawthorne
STATE: New York
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                                                    APPLICATION NUMBER:
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Stinson, Jeffrey R.
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Moyer, Mary B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meins, Jr., Frederick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIBA-GEIGY Corporation
                                   MBER: US 08/042,847
6-APR-1993
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US 07/632,441
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                                                                                                                                                                                                                                                                             US-08-444-803-5/c
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Best Local Similarity 52.1
watches 75; Conservative
                                                                                                                                                                                                                                         Sequence 5, Applic Patent No. 5654414
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FILING DATE: 12 APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 4483 base pairs
                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: US 07/368,672
PTLING DATE: 20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                   4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
                                                                                                                                                                                                                                                                                                                                                                                                                         4421 CAATTCACACGGAGCTAGTTTGTGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT 4362
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
                                                       APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTCTTTCTCTCCCCCTCCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
                                                                                                                                                                                                                                                          Application US/08444803
                                               Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                        Friedrich, Leslie Goodman, Robert M.
                                                                                                                                            Duesing, John H.
                                                                                                                                                                 Beck, James J.
                                    Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                  Alexander, Danny C
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Neuhaus, Jean-Marc
Payne, George B.
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52.1%; Pred. No. 1.1;
ative 0; Mismatches
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                                                                                                                               Leslie B
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APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
EILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
EILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
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FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
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APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Walliams, Shericca C.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
                                                                                                                                                                      APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
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                                                                     FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
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NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
PELECOMMUNICATION INFORMATION:
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19-MAY-1995
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7-SEP-1990
                                                                                                                                               US 08/045,957
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Best Local Similarity 52.1%;
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TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 5
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                                                          ZIP: 1033

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CURRENT APPLICATION UNMBER: US/08/449,043
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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tent No. 5689044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 4483 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                      4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
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                CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                  ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
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                                                                                                                                                                                                                    Hawthorne
: New York
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Stinson, Jeffrey R.
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Payne, George B.
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Meins, Jr., Frederick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beck, James J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ryals, John A
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Montoya, Alice
JMBER: 08/181,271
13-JAN-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leslie B.
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Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                              REGULATABLE AND ANTI-PATHOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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Best Local Similarity
Matches 75; Conserv
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FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION UNBER: US 07/425,504
ENTING DATE: US 07/425,504
ENTING DATE: US 07/425,504
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APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122

FILING DATE: 27-SEP-1991

PRIOR APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4483 base pair
                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                           4421
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FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION TOTAL
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                                                                                                                                                     REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20-JUN-
PRIOR APPLICATION DATA:
4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
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                                121 TIGGITIGIGAATCCATCTIGCTT 144
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                                                                                                  NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                         CAATTCACACGGAGCTAGTTTGTGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT 4362
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ilarity 52.1%;
Conservative
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20-JUN-1989
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·08-456-265A-5/c
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
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APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
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FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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APPLICATION NUMBER: US 0
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                 APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
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APPLICANT: Ryals, John A.
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STATE: New York
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                                                         JMBER: US 07/368,672
20-JUN-1989
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MBER: US 07/329,018
24-MAR-1989
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APPLICANT:
APPLICANT:
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                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                         TITLE OF INVENTION: CH
TITLE OF INVENTION: DN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4421 CAATTCACACGGAGCTAGTTTGTGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT 4362
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Local Similarity 52.1%;
nes 75; Conservative
                                                                                 COUNTRY: UZIP: 10532
                                                                                                              CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                           STREET:
                                                                                                                                           ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
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                                                                                                            New York
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Ward, Eric R.
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Stinson, Jeffrey R.
Uknes, Scott J.
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Meins, Jr., Fred
Montoya, Alice
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Goodman, Robert M.
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                                                                                                                                                                                                         CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                 Jean-Marc
                                                                                                                                                                                                                                        Shericca C.
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   Version #1.25
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CURRENT APPLICATION DATA:

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Best Local
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APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
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PRIOR APPLICATION DATA:
US 07/305,566
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
4481 GCTCTTTTGCTGCTCTGAATAGAGTCTTCTTTCCTGCCTTTGGAGTTGATGAAATGGA 4422
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                          TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07 FILING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/368,672 FILING DATE: 20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08 FILING DATE: 13-JAN-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                     GCTCTTTCTCTCCCCTCCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
                                                                   ch 9.2%;
1 Similarity 52.1%;
75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Elmer, James Scott
                                                                                                                                                                                                                                           4483 base pairs
                                                                                                                                                                                                                                                                                                   (919)
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                                                                                                                                                                                                                                                                                                                                                                 36,129
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                                                                   Score 33.6; DB Pred. No. 1.1; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    S-19825/P1/CGC 1727
                                                                                                   DB 3;
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                                                                    Indels
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                                                                                                                              STREET: / CITY: Hawthorne
CITY: New York
"TATE: New York
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION UNBER: US//8/455,244 FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
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                                                                                  PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T: Williams, Shericca C.
INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08455244
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Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ward, Eric
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Stinson, Jeffrey R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beck, James J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weuhaus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
JMBER: US 07/632,441
21-DEC-1990
                                                   JMBER: US 08/042,847
6-APR-1993
                                                                                                    8-MAR-1988
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                                                                                                                US 07/165,667
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PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER:

20-OCT 1989

US 07/425,504

US 07/848,506

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STRANDEDNESS: sing,
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-455-244-5
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Best Local Similarity 52.1%;
Matches 75; Conservative
                                                                                                                                                                                                                                                       Sequence 5, Applic Patent No. 5804693
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TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 5
                                                                                                         APPLICANT:
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REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
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NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                      Application US/08454876
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                                                                                      Harms, Christian
Meins, Jr., Frederick
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Sperison, Christoph
                                                                                                                      Goodman, Robert M.
                                                                                                                                           Friedrich,
                                                                                                                                                            Duesing, John H.
                                                                                                                                                                                                Alexander, Danny C.
               Neuhaus, Jean-Marc
Payne, George B
                                                    Moyer, Mary B.
                                                                   Montoya, Alice
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Pred. No. 1.
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APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRIOR APPLICATION UDMBER: US 08/042,847

FILING DATE: 6-APR-193

PRIOR APPLICATION DATA:

APPLICATION UDMBER: US 08/042,847

FILING DATE: 6-APR-193

PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
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APPLICANT:
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                                                                                                             APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DAA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-1
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: CIBA-GEIGY Corporation
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APPLICATION NUMBER:
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31-MAY-1995
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7-SEP-1990
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; MOLECULE TYPE:
US-08-454-876-5
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Best Local S
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LENGTH: 4483 base pairs
TYPE: nucleic acid
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
                                        CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                         CITY: Hawthorne
STATE: New York
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            APPLICATION NUMBER: 08 FILING DATE: 13-JAN-94
                                                                        APPLICATION NUMBER: FILING DATE: 31-MA
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                    ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
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Ward, Eric
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Stinson, Jeffrey R.
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Goodman, Robert M.
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Moyer, Mary B.
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Meins, Jr., Frederick
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on, Christoph
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us 08/093,301
                            08/181,271
                                                                                      US/08/457,364
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Best Local S
Matches 75
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NAME: Elmer, James Scott
REGISTRATION UNMBER: 36,129
REFERENCE/DOCKET NUMBER: 5-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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                                                                                                                                          4481 GCTCTTTTGCTGCTCTCTGAATAGAGTCTTCTTTCCTGCCTTTGGAGTTGATGAAATGGA 4422
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FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
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FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4483 base pairs
                                TTGGTTTGTGAATCCATCTTGCTT 144
                                                                       CAATTCACACGGAGCTAGTTTGTGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT 4362
                                                                                                      CATTTCACTGTGATGTATTGTGTTGCAAAAAAAAAAAAGTGTCTTTGTTTAAAATTAC 120
                                                                                                                                                                               GCTCTTTCTCCCCCCCCCCCGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
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6-FEB-1989
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RESULT 12
US-08-456-262-5/c
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APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
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                                                                              APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-CCT 1989
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FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 13-JAN-
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APPLICATION NUMBER: US/08/456,262
FILING DATE: 31-MAY-1995
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APPLICANT:
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APPLICATION NUMBER: (
FILING DATE: 8-MAR-1:
PRIOR APPLICATION DATA:
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FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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ORRESPONDENCE ADDRESS
                                                                   PRIOR APPLICATION DATA:
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              APPLICATION NUMBER: US 07/848,506 FILING DATE: 6-MAR-1992 TOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Stinson, Jeffrey R.
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US 07/768,122
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US-08-456-240-5/c
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Patent No. 585615
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        GENERAL
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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                            APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 7-SEP-1
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: 11r
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les 75; Conserv
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REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
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REGISTRATION NUMBER: 36,
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Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
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                                                                                                                                                                                                                                                                                                    Ryals, John A.
Alexander, Danny C.
                                                                                                                                           Payne, George B.
                                                                                                                                                         Neuhaus, Jean-Marc
                                                                                                                                                                           Moyer, Mary B
                                                                                                                                                                                       Montoya, Alice
                                                                                                                                                                                                        Harms, Christian
Meins, Jr., Frederick
                                                                                                                                                                                                                                        Friedrich, Leslie B. Goodman, Robert M.
                                                                                                                                                                                                                                                         Duesing, John H.
Friedrich, Lesli
                                                                                                                                                                                                                                                                                          Beck, James J
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24-MAR-1989
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20-JUN-1989
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; Pred. No. 1.1;
0; Mismatches
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TELEFAX: (919)541-868
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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APPLICATION NUMBER: US 07/678,378
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                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                         NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993
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FILING DATE: 13-JAN-94
APPLICATION NUMBER: US
FILING DATE: 16-JUL-19
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                                                                                                                    TELEPHONE:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                       ICATION NUMBER: US 07/368,672
NG DATE: 20-JUN-1989
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                                                                                                  (919)541-8689
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24-MAR-1989
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Best Local Similarity
""+"ches 75; Conserve
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MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/455, FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-1994
                                                                                                                                                                            APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
PRIOR P
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APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
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Friedrich, Leslie B.
Friedrich, Robert M.
Jman, Robert M.
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Meins, Jr., Frederick
Montoya, Alice
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Stinson, Jeffrey R.
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31-MAY-1995
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Pred. No. 1.1;
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                                                  Sequence 1, Application US/08455073A Patent No. 5876949
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Best Local Similarity
Matches 75; Conserv
                                  GENERAL INFORMATION:
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                                                                                                                                                                4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER: US 07
FILING DATE: 27-SEP-1991
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FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
APPLICANT: Gideon Dreyfuss
APPLICANT: Mikiko C. Siomi
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                                                                                                                                                                                      121 TTGGTTTGTGAATCCATCTTGCTT 144
                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US (FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 6-FEB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993
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                                                                                                                                                                                                                                                                                                                                                     1 GCTCTTTCTCTCCCCCTCCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
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8-MAR-1988
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                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 33.6;
52.1%; Pred. No. 1.
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; LOCATION:
US-08-455-073A-1
                                                                                                                                                 Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
3262 CAATTCTGCTTAAACATTAGACCATATATTTCAAAGTTTACAAA 3219
                                                                          3322 AAAAAACAAAAGAAAAAAAAAAAAAAGTTGTTATTTGTTAACCGATCTTAGTCTTTTC 3263
                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,073A
FILLING DATE: 31-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yan Zhang
TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods
TITLE OF INVENTION: Of Making And Using The Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                   150 CCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAA 193
                                                                                                                  90 AAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                            : 4362 base pairs nucleic acid EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PA
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220..2118
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                                                                                                                                                                              8.3%;
55.8%;
                                                                                                                                                        Score 30.4; DB 4; Length 4362;
Pred. No. 7.8;
0; Mismatches 46; Indels 0
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Search completed: September 28, 1999, 11:33:07 Job time: 2067 sec

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pir2:JO1191
pir2:A35052
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pir2:A55173
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pir2:JC4057
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pir2:PC1123
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Query: US-09-030-606-115
Query length: 366
Database: PIR_60:*
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pir2:S56969
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-Q=/Cgn2_1/USPTQ_spool/US09030606/runat_24091999_171617_29825/app_query.fasta.1  
-DB-pIR_60 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000  
-MINNATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500  
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR_SCORE=escore -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pfs -NORM-stat -USER-US09030606 -NCPU=6 -ICPU=3 -WAIT
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        2: I48769
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2: C69795
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       | Sip(w7) alpha-chain - mouse (fr
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| hypothetical protein 19 - Agroba
| hypothetical protein CO7A9.10 - hypothetical protein THR088w - outer membrane protein class 3
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hypothetical protein 668 - slim
vanH protein - Enterococcus face
ywbN protein - Bacillus subtili
interleukin-2 receptor beta cha
hypothetical protein YHR032w -
hypothetical protein YBR0726 -
nonstructural protein V - parai
probable sphingolipid transport
nitrate reductase (NADH) (EC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                               I suppressor protein SPT23 - yea probable C-14 sterol reductase adenylosuccinate synthetase - h sucrose synthase (EC 24.1.13) interferon precursor - duck endoflagellar protein ftaB - Le alpha-casein precursor - rat probable membrane protein YMR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein - bloodfil cation-transporting ATPase (EC hypothetical protein ZC84.3 - Chypothetical protein BC84.3 - hypothetical protein PH1534 - Finterleukin 2 receptor beta chalmG307 homolog H08 orf726 - Myco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Documentation
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histone H2A - rat (fragment)
! NADH-ubiquinone oxidoreductase
                                                                                                                                                                                         adenylosuccinate synthase (EC hypothetical protein YDR362c
                                                                                                                                                        adenylosuccinate synthase (EC El protein - human papillomav
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pir2:S75651
pir2:S56681
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hypothetical protein - A
C; Species: Arabidopsis t
   seq_name: pir2:PC1123
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US-09-030-606-115/rev x E71422
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hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C;Accession: E71422
C;Accession: E71422
P.; Wedler, E.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; G
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, M.; Schaeffer, M.; Funk, B
Avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgdomen
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
C.; Chalwatzis, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.; Chalwatzis, N.
A;Tittle: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis A;Reference number: A71400; MUID:98121113
A;Accession: E71422
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1052 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:Z97339; NID:g2244901; PID:e327481; PID:g2244929
C;Genetics:
A;Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||::::::|||:::::|||
323 ThrLysLysH1sLysValLeu.................................
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 ACTTCAAGTCACAGACTTTATGTGACAGATTGGAGCAGGGTTTGTTATG
                                                                                                                                                          113 TAAACAAAGACACTTTTTTTTTTTTGCAACACAATATACATCACAGTGAA
                                                                                                                                                                                                                                                                      163 ACTAGTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                 342 lyLeuGlyGlyAlaSerLeuThrThrAspGlyPheThr......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 ..CTGGGTGAAATGGTTCTGAGAACCATCCAATTCACCTGTCAGATGCTG
ThrCys...ProThrLysLeuGlnGlnAsnArgSerLysTyrArgIleGl
                                                                                                        laAsnLysIleLysPheValGlyLeu...HisAlaValLysGluLysLys
                                                                                                                                                                                                                                                                                                                                                          ATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAGAGATGGGTTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTGTAATCCTTGCAAATTGCAAGTTGAAAGAATTAAATTCAGAGGAGG
                                                                                                                                                                                                                ......GlnGluGlyCysArgLysAspGlyGluSerAspProArgValA
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                                                                                                                                                                                                                                                                                                                     ....ThrLysSerAsnLeu.....
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48.20
48.24
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Gaps:
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6
26.891
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592
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hypothetical protein sill87
beta-fructofuranosidase (EC
  405
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S111879
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doma

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cation-transporting ATPase (EC 3.6.1.-) pacL-2 - Synechocystis sp. (strain PCC 6803)
%;Alternate names: protein s111076
C:Species: Synechocystis sp.
A;Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
C;Accession: S77454
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
                                   A;Cross-references: EMBL:D90905; GB:AB001339; NID:g1652360; PID:d1018034; PID:g1652379 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
Ratio:
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A;Accession: PC1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
hypothetical protein - bloodfluke planorb (fragment)
C;Species: Blomphalaria glabrata (bloodfluke planorb)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
C;Accession: PC1123
A; Gene: pacL: 2
                                                                                                                       A; Molecule type: DNA
A; Residues: 1-972 <KAN>
                                                                                                                                                                                                             A; Reference number: S74322;
A; Accession: S77454
                                                                                                                                                                                                                                                                                  DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-030-606-115 x PC1123
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A; Residues: 1-651 <KNI>
                                                                                                                                                                                  A; Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: pir2:S77454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 sLysLysIleProValValLysThrThrLysPheLeuGlyLeuThrL 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 CysAsnLeuArgGlyLeuHisLeuAsn.....ProGluLeuPheIleHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 AAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 TGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTGTGTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GC......TTTTTCCCCCATTGGAACTAGTCATTAACCCATC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spArgAspThrLeuLeuLeuTyrArgSerLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysGluLeuLysLysGlyGlnLysSerLeuAsnIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGAACTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euAspSerLysPheAsnPheLeuProTyr.......ile
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1.347
51.042
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                                                                                                                                                                                                                                           MUID: 97061201
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Identity:
                                                                                                                                                                                  translation
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5
29.167
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                                                                                                                                                                                  not shown
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alignment_block:
US-09-030-606-115/rev x S28293
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A;Residues: 1-643 <THO>
A;Cross-references: EMBL:Z19157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 2C84.3 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #tC;Accession: S28293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 141/2; 167/3; 245/3; 341/2; 412/3; 600/3; 640/3
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Percent Similarity:
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                                                                                                                                                     870
                          163
                                                                                                           213 ATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAGAGATGGGTTAATG 164
                                                                                                                                                                                                                                                                           291 AATTTATTAAACAGGATAGAAACAGGCTGTCTGGGTGAAATGGTTCTGAG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       886 lIleValAlaCysGlnAspGlyAsnValPheAlaCysArgSerGluArgT 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
ACTAGTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTT 114
                                                               euArgLeuAlaLeuAlaLysLeuPhe....AlaArgLysAlaAlaGlu
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                                                                                                                                                                                          ......AACCATCCAATTCACCTGTCAGATGCTG 214
                                                                                                                                                                                                                                      AsnCysLeuAsnArgLeuLeuSerAspAlaSerAsnThrMetValLeuGl 171
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1.226
51.456
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alignment_scores:
Quality:
Ratio:
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A; Residues: 1-730 <THO>
A; Cross-references: EMBL: Z19157
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                                             seq_name: pir2:D71030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 77/3; 120/3; 213/1; 228/2; 254/3; 332/3; 428/2; 499/3; 687/3; 727/3
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C;Species: Caenorhabditis elegans
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 30-Sep-1993
C;Accession: S28294
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 uIleTyrSerIlePheValArgThrHisSerSerArgLeuSerGluTrpL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 AsnCysLeuAsnArgLeuLeuSerAspAlaSerAsnThrMetValLeuGl 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
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                                                                                                                                                                                                                                                                                            306 eu.....GluCysPhe....
                                                                                                                                                                                                                                                                                                                                             113 TAAACAAAGACACTTTTTTTTTTTTGCAACACAATATACATCAC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 AATTTATTAAACAGGATAGAAACAGGCTGTCTGGGTGAAATGGTTCTGAG
                                                                                                                                                                                              316 ValThrValCysGluLeuMetCysAspProIleHisLeuMetValProLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                              332 sAlaArg 334
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                                                                                                                                                                                                                                                                                                                                                                                                                      ACTAGTTCCAATGGGGAAAAAAGCAAGATGGATTCACAAAACCAAGTAATTT 114
                                                                                                                                                                                                                                                                                                                                                                                          Thr.LeuProAsnThrLysLysGlnIleGlyHisThrLeuAsnValIleL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValThrValCysGluLeuMetCysAspProIleHisLeuMetValProLy 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eu.....GluCysPhe.......AsnAlaHisHisGlnLeu 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thr.LeuProAsnThrLysLysGlnIleGlyHisThrLeuAsnValIleL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....AGTGAAATGTGTAATCCTTGCAAATTGCAAGTTGAAAG 32
                                                                                                                                           AATTAAA 25
                                                                                                                                                                                                                                            .....AGTGAAATGTGTAATCCTTGCAAATTGCAAGTTGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.00
1.226
51.456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....AACCATCCAATTCACCTGTCAGATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity:
                                                                                                                                                                                                                                                                                            .AsnAlaHisHisGlnLeu 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.981
                                                                                                                                                                                                 332
                                                                                                                                                                                                                                                                                                                                             70
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A; Note: sequ
A; Note: sequ
C; Keywords:
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A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
A;Accession: D71030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein PH1534 - Pyrococcus horikoshii c;Species: Pyrococcus horikoshii c;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998 C;Paccession: D71030
                                                                                                                                                                                                                                                                                                                                                         R;Page, T.H.; Dallman, M.J.
Eur. J. Immunol. 21, 2133-2138, 1991
A;Title: Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha and A;Reference number: A46535; MUID:91364784
A;Accession: B46535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: B46535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
interleukin 2 receptor beta chain - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: pir2:B46535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
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A;Residues: 1-136 <KAN
A;Residues: 1-136 <KAN
A;Cross-references: GB:APO00006; NID:g3236133; PID:d1031587; PID:g3257961
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa
                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-537 < PAG>
                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: D71030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 TIGGATGGTTCTCAGAACCATTTCACCCAGACAGCCTGTTTCTATCCTGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 GAAAAACATCTGAAGAGCTAGTCTA....TCAGCATCTGACAGGTGAA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 TCCCCATTGGAACTAGTCATTAACCCATCT.....CTGAACTGGTA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 TTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 ThrProValGluThrAlaIleHisProSerPheSerLeuLeuHisTrpAl 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 leGlyPheThrProValGlnThrSerProLeuGlyThrThrMetHisAla 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 aSerAsnIleAspProSerAsnIleArgProSerSerIleAspLysIleI 58
                                                                                                                                                                            sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:60818, NCBIP:60819) rds: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PH1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerLeuSerMetGlyGlyPheThrIleLeuIleThrAsnPro
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                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.50
1.671
59.375
   63.00
1.212
44.444
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Gaps: 2
Percent Identity: 31.250
Percent Identity: 25.641
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alignment_block: US-09-030-606-115/rev x B46535

beta

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RHIMMELIECICH. R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. RHIMMELIECICH. R.; Hilmeliecich. R.; Hilbert, J. 1996
A.Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A:Reference number: S73327; MUID:97105885
A:Accession: S73727
A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA
A:Residues: 1-726 (HIM)
A:Residues: 1-726 (HIM)
A:Ross-references: EMBL:AE000039; GB:U00089; NID:g1674082; PID:g1674084
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
MG307 homolog H08_orf726 - Mycoplasma pneumoniae (ATCC 29342) (SGC3)
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 17-Jul-1998
C;Accession: S73727
                                                                                                                                                                                                                                                                                                                                         alignment_block:
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A;Genetic c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: pir2:S73727
                                                                                                                                                                                                                                                           Align seg 1/1 to: S73727 from: 1 to: 726
                                                                                                                                                                                                                                                                                                                 US-09-030-606-115/rev x S73727
                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                651 ySerAspLysIleThrTyrLeuGlnPheSerTyrLysAspIleAspGlyL
                                                                                                                                             129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
                                                                                                   218 TGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAGAGATGGGT 169
                                                                                                                                                                                                        268 AGGCTGTCTGGGTGAAATGGTTCTGAGAACCATCCAATTCACCTGTCAGA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 uLysAlaSerSerProSer.ProSerGlyHisSerGlnAlaSerCysPhe 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 ValleuAspArgAspSerLysThrMetGlnMetLeuLeuPheGlnLysGl 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 InSerPhePheSerProThrGlySerAlaProGluIleSerProLeuGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 ......GAGAACCATCCAATTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
TA...ATGACTAGTTCCAATGGGGAAAAAGCAAGATGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATACATCACAGTGAAATGTGT.....AATCCTTGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrAsnGln......GlyTyrPhePhePheHisLeuSerAs 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCAAGATGGA...TTC
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suppressor protein SPT23 - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein YKL020c
C:Species: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 10-Jul-1998
C:Accession: S37837; S40696
seq_name: pir2:JC4057
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US-09-030-606-115/rev x S37837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 11L C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology F; 742-774/Domain: ankyrin repeat homology <a href="AN1">AN1</a>>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: SGD:SPT23
A;Cross-references: SGD:S0001503; MIPS:YKL020c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 136-714,'P',716-737,'ERKIYLVLLATYGVY' <BUR>
A;Cross-references: EMBL:L24760; NID:g404815; PID:g404817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Molecular characterization of the SPT23 gene: a dosage-dependent suppressor A;Reference number: S40695; MUID:94262317 A;Accession: S40696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1082 <RIE>
A;Residues: 1-1082 <RIE>
A;Cross-references: EMBL:228020; NID:g486010; PID:g486011; MIPS:YKL020c
A;Experimental source: strain S288C
R;Burkett, T.J.; Garfinkel, D.J.
Yeast 10, 81-92, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Rieger, M.
submitted to the Protein Sequence Database, March 1994
s;Reference number: $37832
A;Accession: $37837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ArgIleArgAsnAlaHisAlaArgLysAsnPhePheIleHisLeu...Pr 156
                                                      223
                                                                                                                                                          210 CysAsnArgCys..
                                                                                                                                                                                                                                                                                                                                                                                   176 rIleProAsnArgAspIleAsnGluArgThrLeuPheLeuAspAlaPheL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                       118 AATTTTAAACAAAGAC.....ACTTTTTTT.....TTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 TGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAGAGATGGGT
                                                                                                                                                                                                                                                                                                                                   68
                                                                                                         10 GAGAAAGAGC 1
                                                                                                                                                                                                                   60 TGTAATCCTTGCAAATTGCAAGTTGAAAGAATTAAATTCAGAGGAGGGGA 11
                                                                                                                                                                                                                                                                                                                    TG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAATGACTAGTTCCAATGGGGAAAAAAGCAAGATGGATTCACAAACCAAGT 119
                                                   gArgLysSer 226
                                                                                                                                                                                                                                                                       euLeuCysAlaSerAsnAsnAsnSerAsnAsnPheLysGlnThrTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oSerAspCysIleAlaLysAspLysPhePhe.ThrSerSer......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCTGTCTGGGTGAAATGGTTCTGAGAACCATCCAATTCACCTGTCAGA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.50
1.157
51.923
                                                                                                                                                                                                                                                                                                                             ....CAACACAATATACATCACAGTGAAATG 61
                                                                                                                                                                IleAsnArgGluLysArgArgAlaSerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 30.769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
                                                                                                                                                                                                                                                                            209
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adenylosuccinate synthetase - human c; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Nov-1995 C; Accession: S21166 R; Powell, S.M.; Zalkin, H.; Dixon, J.E. FEBS Lett. 303, 4-10, 1992 A; Title: Cloning and characterization of the cDNA encoding human adenylosucce. A; Reference number: S21166; MUID:92275078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
probable C-14 sterol reductase (EC 1.1...) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 29-Unn-1995 #sequence_revision 14-Jul-1995 #text_change 13-Sep-1998
C;Accession: JC4057
R;Smith, S.
Gene 155, 139-140, 1995
A;Title: Cloning and sequence analysis of an ERG24 homolog from Schizosaccharomyces pomb
A;Reference number: JC4057; MUID:95212923
A;Accession: JC4057; MUID:95212923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: erg24
C;Reywords: oxidoreductase
                                                                                                                                                                                                                                                                       A:Molecule type: mRNĀ
A;Residues: 1-455 <POW>
A:Cross-references: EMBL:X66503
C:Superfamily: adenylosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: $21166
                                                 alignment_block:
US-09-030-606-115/rev x S21166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:S21166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-030-606-115/rev x JC4057
                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L36039; NID:g703463; PID:g703464
     Align seg 1/1
                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 nPheLeuGlyTyrTyrIlePheArg......GlyAlaAsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 lyGlnLysAsnArgPheArgSerAsnProAsnAspProLysLeuLysHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 GGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTTTAAACAAAGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 ....ATGTTTTTCTACCAGTTCAGAGATGGGTTAATGACTAGTTCCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 HisProValAspLeuGlyLeuValLysThrLeuAlaIleLeuCysLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 CATCCAATTCACCTGTCAGATGCTGATAGACTAGCTCTTCAG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 TTTTTTTTTTTGCAACACAA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuLysPheIleGlnThrLys 338
                                                                                                                                                                               Quality:
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6
       S21166
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                                                                                                                              61.50
1.538
62.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.50
1.809
59.649
  from: 1
                                                                                                                         Length: 64
Gaps: 2
Percent Identity: 31.250
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     е
6
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: Identity:
     455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  human adenylosuccinate synthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197
seq_documentation_block:
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C:Accession: S19125
R;Chopra, S.; Del-favero, J.; Dolferus, R.;
Plant Mol. Biol. 18, 131-134, 1992
A;Title: Sucrose synthase of Arabidopsis: ge
A;Reference number: S19125; MUID:92119221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase F;276-750/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-804 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana
sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: S19125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-030-606-115 x YUMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 31/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428/3; 484/2; 559/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir1:YUMU
seq_name: pir2:S57642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: YUMU from: 1 to: 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                        307 CATGCATAACAAACCCT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673 PheGlyLeuThrValValGluSerMetThrCysAlaLeuProThrPheAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 uAlaGluLysAsnValGlnLysGly...LysGlyLeuGluGlyTrpGluL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 AACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGAAGAGCT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 TTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCCC...ATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 AlaAlaAspGlyIleGlnGluGlnArgGlnGluGlnAla 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TTCAGAGATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ysArgLeuIleIleSerAspArgAlaHisIleValPheAspPheHisGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 TTCACCTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAG
                                                                                                                                                                  712 sProAspGlnValAlaGlySerLeuAlaLeu.
                                                                                                                                                                                                                      257 CCCAGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTA 306
                                                                                                                                                                                                                                                                                                                                207 AGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 ACAGGATAGAAACAGGCTGTCTGGGTGAAATGGTTCTGAGAACCATCCAA
                                                                                                                                                                                                                                                                                                                                                                                      aThrCysHisGlyGlyProAlaGluIleIleGluAsn.......
                                                         hrCysAsnThrAsnPro
                                                                                                                                                                                                                                                                            ......GlyValSer.GlyPheHisIleAspProTyrHi
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: X60987; NID: g16525; PID: g16526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.50
1.577
53.425
                                                         730
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4
28.767
                                                                                                                                                                  PheGluT
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                                                                                                                                                                                                                                                                               712
                                                                                                                                                                                                                                                                                                                                  256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     689
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                                                                                                                                                                                                                                                                                                                                                                                      701
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alignment_block:
US-09-030-606-115/rev x A44814
                                                                                                                                                                                                                               A;Gene: flaB
C;Superfamily: flagellin
                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A44814
R. Rod, J.I.; Faine, S.; Adler, B.
R. Mitchison, M.; Rodd, J.I.; Faine, S.; Adler, B.
R. Gen. Microbiol. 137, 1529-1536, 1991
A;Title: Molecular analysis of a Leptospira borgpetersenii gene encoding an endoflagella A;Reference number: A44814; MUID:92065222
A;Accession: A44814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endoflagellar protein ftaB - Leptospira borgpetersenii
C:Species: Leptospira borgpetersenii
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Feb-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <SCH>
A:Cross-references: EMBL:X84764; NID:g886834; PID:g886835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon precursor - duck
C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 10-Sep-1997
C;Accession: S57642
R;Schultz, U; Koeck, J; Schlicht, H.J.; Staeheli, P.
submitted to the EMBL Data Library, February 1995
A;Description: Recombinant duck interferon: a new reagent to study the mode of interferon
                                                                                                                                 alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-283 <MIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-030-606-115/rev x S57642
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A; Accession: S57642
                                                                                                                                                                                                                                                                                                                  A; Note: sequence extracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:A44814
                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                             Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 isAsp.LeuLeuAsnGln......LeuGlnHisHisIleHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 CAAGTAATTTTAAACAAAGACACTTTTTTTTTTTTTTGCAACACAATATACA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 AATGACTAGTTCCAATGGGGAAAAAGCAAGATGGATTCAC.....AAAC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 GCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAGAGATGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCACAGTGAAATGTGTAATCCTTGCAAATTGCAAGTTGAAAGAATTAAAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaAlaHisThrAlaLeuHisLeuLeuGlnHisLeuPhe...AspThrLe 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rgArgGly 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sHisLeuGluArgCysPheProAla....AspAlaAlaArgLeuHisA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 u.....SerSerProSerThrProAlaHisTrpLeuHisThrAlaArgH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.00
1.452
60.000
                                                                              61.00
1.848
66.000
                                                                                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 70
Gaps: 6
Percent Identity: 35.714
                                                                                Percent
                                                                                                                                                                                                                                                                                                                  NCBI backbone (NCBIN:66827, NCBIP:66829)
                                                                                Identity:
                                                                                1
28.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123
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A:Introns: 17/3; 28/3; 37/3; 52/3
C;Superfamily: Alpha-sl-casein
C;Keywords: mammary gland; milk; phosphoprotein
E;1-15/Domain: signal sequence #status predicted
E;16-284/Product: alpha-casein #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J00710

R;Yu-Lee, L.Y.; Richter-Mann, L.; Couch, C.H.; Stewart, A.F.; Mackinlay, A.G.; Rosen, Nucleic Acids Res. 14, 1883-1902, 1986

A;Title: Evolution of the casein multigene family: conserved sequences in the 5' flan A;Reference number: A23514; MUID:86148515

A;Accession: A23514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hobbs, A.A.; Rosen, J.M.
Nucletc Acids Res. 10, 8079-8098, 1982
A;Title: Sequence of rat alpha- and gamma-casein mRNAs: evolutionary comparison
A;Reference number: A93452; MUID:83143278
A;Accession: A03105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-casein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Aug-1996
C;Catession: A03105; A23514
                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-030-606-115/rev x KART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
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C;Genetics:
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A; Residues: 1-52 < YUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-284 < HOB>
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Percent Similarity:
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                                                                                                                                 189 TCTACCAGTTCAGAGATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 ValAspGluValAspArgIleAlaSerGlnAlaGluPheAsnLysPheLy 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 CTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAG 177
                                                         89 TGCAACACAATATACATCACAGTGAAATGTGTAATCCTTGCAAATTG 43
euGlnArgGlnIleLysTyrSerGlnLeuLeuGlnGlnAlaSerLeu
                                                                                                          nLysAsnIleAlaAsnLysGluIleLeuAsnArgCysThrLeuGluGlnL
                                                                                                                                                                                                          SerSerSerGluGluSerLysAspAlaIleProSerAlaThrGluGl
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Swissprot_37: SUS2_ARATH +
Swissprot_37: INF_NARAL -
Swissprot_37: INF_CAREL -
Swissprot_37: RAS2_DROME -
Swissprot_37: RS25_DROME -
Swissprot_37: RY36_YEAST -
Swissprot_37: VASH_ENTFC -
Swissprot_37: VASH_ENTFC -
Swissprot_37: YASH_BOUSE -
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Query: (US-09-030-606-115
Query length: 366
Database: SwissProt_37:*
Database sequences: 77977
Database length: 28268293
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SwissProt_37:YN83_CAEEL -
SwissProt_37:YN83_CAEEL -
SwissProt_37:SP3_YEAST
SwissProt_37:SP3_YEAST
SwissProt_37:PURA_HUMAN -
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Swissprot_37:NY4R_MOUSE
Swissprot_37:RPC1_PLAFA
Swissprot_37:TAMI_POVHA
Swissprot_37:KROS_AVISU
Swissprot_37:KROS_CHICK
Swissprot_37:XC19_GUITH
Swissprot_37:XC19_GUITH
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Swissprot_37:YKTO_CAEEL+
Swissprot_37:YKTO_CAEEL+
Swissprot_37:YHO8_YEAST-
Swissprot_37:SPL1_CAMA+
Swissprot_37:SPL1_CAMA+
Swissprot_37:INV2_DAUCA-
Swissprot_37:INV2_DAUCA-
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-Q-/cgn2_1/USPTO_spool/US09030606/runat_24091999_171618_29883/app_query.fasta.l
-DB-Sw1ssprot_37 -QFMT-fastan -SUFFIX-rsp -GAPOP-12.000
-GAPEXT=4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -YGAPOF-10.MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-escore
-ALIGN-15 -MODE-LOCAL -OUTFYT-pfs -NORM-stat -USER-US09030606
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Len | Documentation | Chicken | Gll | Q09660 gallus gallus (chicken | 730 | Q09660 gallus gallus (chicken | 730 | Q09660 gallus norvegicus (rat) | P26896 rattus norvegicus (rat) | 1082 | P35210 saccharomyces cerevi | 455 | P35210 saccharomyces (da | P00611 rattus norvegicus (rat) | 3672 | Q09017 arabidopsis thaliana | 191 | P51526 anas platyrhynchos (da | 284 | P02661 rattus norvegicus (rat) | 3672 | Q01313 | Caenorhabditis elegal | 113 | P48588 drosophila melanogast | 1785 | Q04952 saccharomyces cerevi | 586 | P46982 saccharomyces cerevi | 581 | P39597 bacillus subtilis. | hy | 539 | P16297 mus musculus (mouse) | 581 | P38767 saccharomyces cerevi | 581 | P38767 saccharomyces cerevi | 581 | P38767 saccharomyces cerevi | 582 | P4061297 mus musculus (mouse) | 581 | P4061297 mus musculus (mouse) | 581 | P4061297 mus musculus (mouse) | 582 | P4061297 mus musculus (mouse) | 583 | P51867 bos taurus (bovine) | 583 | P40662 drosophila melanogast | 409 | P4013 saccharomyces cerevis | 663 | P46664 mus musculus (mouse) | 663 | P55439 bovine adenovirus ty | 10023 caenorhabditis elegan | 254 | P34821 caenorhabditis elegan | 254 | P38805 saccharomyces cerevis | 20869 | P38805 saccharomyces | 20869 
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SwissProt_37:CTRO_MOUSE -
SwissProt_37:YAG1_YEAST +
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                                                                                                                                                                                                                                                                                                                    US-09-030-606-115 x IAP_CHICK
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FUNCTION: APOPTOTIC
                                              ....TACACATTTCACTGTGATGTATAT
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                                                                                                               SerProLeuLeuAlaSerValMetLysGlnAsnAlaHisCysGlyGluLe
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Percent Identity: 24.432
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Q90560;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INHIBITOR OF APOPTOSIS PROTEIN (IAP) (INHIBITOR OF
                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIGBY M.R., KIMPTON W.G., YORK J.J., "ITA, a vertebrate homologue of IAP t lymphocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.

TISSUE SPECIFICITY: CELLS OF THE TEXMPHOCYTE LINEAGE. FOUND I
BOTH CORTICAL AND MEDULARY CELLS OF THE THYMUS.

DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS
T-CELL ACTIVATION IN SPLEEN AND THYMUS.

SIMILARITY: MEMBER OF THE IAP FAMILY.

SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
ADOPTOSIS PROTEIN REPEAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                              PS01282; BIR_REPEAT;
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APOPTOTIC SUPPRESSOR (BY SIMILARITY).
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56.50 97.69 43.83
56.00 107.86 45.57
                     REPEAT; NUCLEAR PROTEIN.
BIR REPEAT 1.
BIR REPEAT 3.
BIR REPEAT 3.
C3HC4-TYPE.
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CRC32;
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417 i P39713 saccharomyces
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01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-UN-1994 (REL. 29, LAST ANNOTATION UPDATE)
HYPOTHETICAL 80.7 KD PROTEIN 2C84.3 IN CHROMOSOME
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                                                                                                                                           WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET J., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTHORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
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EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHAI
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MEDLINE; 94150718.
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                                                                            NATURE 368:32-38(1994)
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seq_documentation_block:
ID IL2B_RAT STANDARD;
AC P26896;
DT 01-AUG-1992 (REL. 23, LAST
DT 01-EB-1996 (REL. 33, LAST
DT 01-EB-1996 (REL. 33, LAST
DT 01-EB-1996 (REL. 33, LAST
DE INTERLEUKIN-2 RECEPTOR BET
DE (HIGH AFFINITY IL-2 RECEPT
GN IL2RB.
OC RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDA
OC RODENTIA; SCIUROGNATHI; MU
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91364784.
RA PAGE T.H., DALLMAN M.J.;
RT "MOJECULAR CHORDA
RT and beta chain genes: diff
RT response to mitogenic stim
RL EUR. J. IMMUNOL. 21:2133-2
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US-09-030-606-115/rev x YN83_CAEEL
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PIR; S28293; S28293; S28293; S28293; S28293; CE15022.
WORMPEP; ZC84.3; CE15022.
HYPOTHETICAL PROTEIN.
SEQUENCE 730 AA; 80739 !
  SEQUENCE FROM N.A.
MEDLINE; 913647944.
MEDLINE; DALLMAN M.J.;
PAGE T.H., DALLMAN M.J.;
"Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha and beta chain genes: differentially regulated gene activity in response to mitogenic stamulation.";
EUR. J. IMMUNOL. 21:2133-2138(1991).
                                                                                                                                                                        RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                      01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 sAlaArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 ATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAGAGATGGGTTAATG
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                                                                                                                                                                                                                                                     LALEGALANTZ RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122).
ILDRB.
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alignment_block:
US-09-030-606-115/rev x IL2B_RAT
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DISULFID
CARBOHYD
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DOMAIN
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SIGNAL
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                                      362 ThrAsnGln...........GlyTyrPhePhePheHisLeuSerAs
                                                                               DOMAIN
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                                                                                                                       uLysAlaSerSerProSer.ProSerGlyHisSerGlnAlaSerCysPhe
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SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN.
                                                                                                                                                                                                                                               CTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAG 177
                                                                                                                                                                                                                                                                                        lnSerPhePheSerProThrGlySerAlaProGluIleSerProLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
  TATACATCACAGTGAAATGTGT.....
                                                                                                                                                              AGATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCAAGATGGA...TTC 130
                                                                                                                                                                                                      ValLeuAspArgAspSerLysThrMetGlnMetLeuLeuPheGlnLysGl
                                                                                                                                                                                                                                                                                                                                                                     rSerGlnH1sGlyGlyAspLeuGlnLysTrpLeuSerSerProValProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                            ......GAGAACCATCCAATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.00
1.212
44.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERLEUKIN-2 RECEPTOR BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA6DAB6E CRC32;
Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 641
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                                          373
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                                                                                                                                                                                                                                                                                                                                                                                                                245
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alignment_block:
US-09-030-606-115/rev x SP23_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: SwissProt_37:SP23_YEAST
                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                      Align seg 1/1 to: SP23_YEAST
                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                              EMBL; 228020; G486011; -
EMBL; L24760; G404817; A
PIR; S37837; S37837;
SGD; L0002041; SPT23.
PFAM; PF00023; ank; 2.
CONFLICT 715
SEQUENCE 1082 AA; 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: DOSAGE-DEPENDENT SUPPRESSOR OF TY-INDUCED PROMOTER MUTATIONS. MAY EXERT IT SUPPRESSION EFFECT THROUGH PROTEIN-PROTEIN INTERACTIONS SINCE DOES NOT PRESENT ANY OF THE MOTIFS GENERALLY FOUND IN TRANSCRIPTIONAL ACTIVATIONS OR DNA BINDING PROTEINS.
-I- SIMILARITY: TO YEAST YIRO33W.
-I- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 738
ONWARD AND IS SHORTER (752 AA) DUE TO A FRAMESHIFT.
                                                                  218 TGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAGAGATGGGT 169
                                                                                                   141 ArgIleArgAsnAlaHisAlaArgLysAsnPhePheIleHisLeu...Pr 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BURKETT T.J., GARFINKEL D.J.;
"Molecular characterization of the SPT23 gene: a dosage-dependent suppressor of Ty-induced promoter mutations from Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPT23 PROTEIN.
SPT23 OR YKL020C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (REL.
01-JUN-1994 (REL.
01-FEB-1995 (REL.
                                156 oSerAspCysIleAlaLysAspLysPhePhe.ThrSerSer...... 169
                                                                                                                                     268 AGGCTGTCTGGGTGAAATGGTTCTGAGAACCATCCAATTCACCTGTCAGA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerevisiae.";
YEAST 10:81-92(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P35210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SP23_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94262317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 136-752 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAATGACTAGTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGT 119
                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                          62.50
1.157
51.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28, CREATED)
29, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                 15 H H 121337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALT_FRAME.
                                                                                                                                                                         from: 1 to: 1082
                                                                                                                                                                                                                                                          Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                   FE9D5306 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                 P (IN REF.
                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1082 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UPDATE)
                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                              30.769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389
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                                                                                                                                                                                                                  PROSITE; PROSITE;
PURINE BIOSYNTHESIS; LIGASE; GTP-BINDING.
NP_BLND

38

44

GTP (POYENTIAL).
ACT_SITE

172

172

BY SIMILARITY.
SEQUENCE, 455 AA; 49915 MW; 28632370 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (REL. 25, CREATED)
01-NOV-1995 (REL. 32, LAST SEO
01-CCT-1996 (REL. 34, LAST ANN
ADENYLOSUCCINATE SYNTHETASE (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                         PFAM: PF00709: Adenylsucc_synt; 1.
HSSP: P12283: 1ADI.
                                                                                                                                                                                                                                                                             EMBL; X66503; G415849;
PIR; S21166; S21166.
MIM; 103060; -.
                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE DE NOVO PATHWAY OF PURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POWELL S.M., ZALKIN H., DIXON J.E.; "Cloning and characterization of the cDNA encoding adenylosuccinate synthetase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PURA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CYTOPLASMIC, AND PARTICULATE FRACTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE BIOSYNTHESIS.

CATALYTIC ACTIVITY: GTP + IMP + L-ASPARTATE = GDP
ORTHOPHOSPHATE + ADENYLOSUCCINATE.

PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gArgLysSer 226
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                                                                                                                                                                                                            PS00513; ADENYLOSUCCIN_SYN_2; PS01266; ADENYLOSUCCIN_SYN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92275078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
HETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMINIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
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alignment_block:
US-09-030-606-115/rev x PURA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: SwissProt_37:SUS2_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: PURA_HUMAN from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                             "Sucrose synthase of Arabidopsis: genomic cloning and sequence characterization.";
PLANT MOL. BIOL. 18:131-134(1992).
-I- FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE AND FRICTOSE FOR VARIOUS METABOLIC PATHWAYS.
-I- CATALYTIC ACTIVITY: UDP-GLUCOSE + D-FRUCTOSE - UDP + SUCROSE.
-I- INDUCTION: BY ANAEROBIC STRESS.
-I- SIMILARITY: TO OTHER PLANTS SUCROSE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
SUCROSE SYNTHASE (EC 2.4.1.13) (SUCROSE-UDP GLUCOSYLTRANSFERASE).
ARABIDOPSIS THALLANA (MOUSE-EAR CRESS)
EUKARYOTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    PFAM; PF00534; Glycos_transf_1; 1.
PFAM; PF00862; Sucrose_synth; 1.
TRANSFERASE; GLYCOSYLTRANSFERASE; MULTIGENE FA
SEQUENCE 804 AA; 91989 MW; 9B980B3B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 TTCACCTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 ACAGGATAGAAACAGGCTGTCTGGGTGAAATGGTTCTGAGAACCATCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 ATTGGAGCAGGGTTTGTTATGCATGTAGAGAACCCAAACTAATTTATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAGAGATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysArgLeuIleIleSerAspArgAlaHisIleValPheAspPheHisGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uAlaGluLysAsnValGlnLysGly...LysGlyLeuGluGlyTrpGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleGlyAsnGlyValValIleHisLeu.....ProGlyLeuPheGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S., DEL-FAVERO J.,
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                           FAMILY
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alignment_scores:

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Percent Similarity:
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                              DISULFID
DISULFID
DISULFID
                                                                                    CYTOKINE;
SIGNAL
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
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                                                                                                               PFAM; PF00143; interferon;
HSSP; P01574; 1AU1.
                                                                                                                                                                                                                                                                                                                                   "RECOMDITE U., KOECK J., SCHLICHT H.J., STAEHELI P.;
"Recombinant duck interferon: a new reagent for studying the mode of interferon action against hepatitis B virus.";
VIROLOGY 212:641-649(1995).
-!- INDUCTION: BY VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANAS PLATYRHYNCHOS (DOMESTIC DUCK).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; ANSERIFORMES; ANATIDAE; ANAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 AACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAAACATCTGAAGAGCT
                                                                        CHAIN
                                                                                                                                             PROSITE; PS00252; INTERFERON_A_B_D;
                                                                                                                                                             EMBL; X84764; G886835; -
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96010237.
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERFERON PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGCATAACAAACCCT 323
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                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY.
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                                                                                                   ANTIVIRAL; GLYCOPROTEIN;
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Percent Identity: 28.767
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BY SIMILARITY.
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seq_documentation_block:
ID CASI_RAT STANDS
AC PO2661;
DT 21-JUL-1986 (REL. 01.)
DT 21-JUL-1996 (REL. 01.)
DT 21-JUL-1996 (REL. 01.)
DT 01-NOV-1997 (REL. 35.)
DE ALPHA CASEIN PRECURS
GN CSNA:
OS RATTUS NORVEGICUS (RU
CCNA:
OC RODENTIA; SCIUROGNATI
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 83143278.
RA HOBBS A.A., ROSEN J.!
RT "Sequence of rat alpl
COMPARTSON of the cal
RI COMPARTSON of the cal
RI COMPARTSON OF TACTOR
RY SEQUENCE OF 1-52 FROI
RY MEDLINE; 86148515
RA WILLEE L.Y., RICHTER
RA MACKINLAY A.G., ROSE.
RT "EVOLUTION of the cal
RT S'FIRIKING and exon
RL NUCLEIC ACIDS RES. 1.
CC -1-FUNCTION: IMPORT
CC -1-SIMILARITY: BELO
CC -1-SIMILARITY: BELO
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CC Use by non-profit
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CC entities requires a
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US-09-030-606-115/rev x INF_ANAPL
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                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                          CALCIUM PHOSPHATE.
-i- SUBCELLULAR LOCATION: EXTRACELLULAR.
-i- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-i- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                     MACKINLAY A.G., ROSEN J.M.;
"Evolution of the casein multigene family: conserved sequences in 5' flanking and exon regions.";
NUCLEIC ACIDS RES. 14:1883-1902(1986).
-i- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOBBS A.A., ROSEN J.M.;
"Sequence of rat alpha- and gamma-casein mRNAs: evolutionary comparison of the calcium-dependent rat casein multigene family.";
NUCLEIC ACIDS RES. 10:8079-8098(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 sHisLeuGluArgCysPheProAla.....AspAlaAlaArgLeuHisA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 isAsp.LeuLeuAsnGln.....LeuGlnHisHisIleHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 AATGACTAGTTCCAATGGGGAAAAAAGCAAGATGGATTCAC....AAAC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                               YU-LEE L.Y., RICHTER-MANN L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-52 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 TCACAGTGAAATGTGTAATCCTTGCAAATTGCAAGTTGAAAGAATTAAAT
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Percent Identity:
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                                                     There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MAMMALIA; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
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35.714
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US-09-030-606-115/rev x CAS1_RAT
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Quality:
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D_LML2_CAEEL STANDARD; PRT; 3672 AA.

C_Q21313;

T_01-NOV-1997 (REL. 35, CREATED)

T_01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

I_01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

LAMININ-LIKE PROTEIN K08C7.3 PRECURSOR.
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Percent Similarity:
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EMBL; X03585; 6736286; -.
EMBL; X03586; E10128; -.
EMBL; X03587; E10129; -.
EMBL; X03587; E10130; -.
PIR; A03105; KART.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1
PFAM; PF00363; CASEIN_S; 1.
MILK; PHOSPHORYLATION; REPEAT; SIGNAL.
    CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
"RHĄBDĮTTĮNA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
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SEQUENCE FROM N.
STRAIN-BRISTOL 1
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WORMPEP; K08C7.3; CEG06136.

PROSITE; PS00022; EGF_1; 19.

PROSITE; PS01186; EGF_2; 4.

PROSITE: PS01248; LAMININ_TYPE_EGF;

PROSITE: PS01248; LAMININ_TYPE_EGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02468
HYPOTHETICAL
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-i- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (1-
-i- SIMILARITY: CONTAINS 21.5 LAMININ EGF-LIKE DOMAIN (1-
-i- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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or send an email to license@isb-sib.ch).
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LAMININ EGF-LIKE 2
LAMININ EGF-LIKE 3
LAMININ EGF-LIKE 4
LAMININ EGF-LIKE 5
LAMININ EGF-LIKE 5
LAMININ EGF-LIKE 6
LAMININ EGF-LIKE 6
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Percent Similarity:
          This SWI
                                                                                STRAIN-SZBRC / AB972;

STRAIN-SZBRC / AB972;

CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;

CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;

SUBMITTED (APR-1995) TO EMBL/GENBAK/DDBJ DATA BANKS.

-I- CATALYTIC ACTIVITY: UDP-GLUCOSE + (1,3-BETA-D-GLUCOSYL)(N) = UDP-GLUCOSYL)(N+1).

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-I- SIMILARITY: STRONG, TO GLS1 AND GLS2.
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Q04952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE 1,3-BETA-GLUCAN SYNTHASE COMPONENT (
GLUCAN-UDP GLUCOSYLTRANSFERASE).
YMR306W OR YM9952.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
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SWISS-PROT entry is copyright. It is produced through a collaboration ear the Swiss Institute of Bioinformatics and the EMBL outstation -
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TO THE S25E FAMILY OF RIBOSOMAL PROTEINS
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alignment_scores:
Quality:
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                  OBERMAIER B., PIRAVANDI E., RINKE M., DOMI SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ -!- SIMILARITY: TO YEAST TTP1.
                                                                                     EUKARYOTA; FUNGI; ASCOMYCETES; SACCHAROMYCETACEAE; SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                  01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 67.3 KD PROTEIN IN SWE1-ATP12 INTERGENIC
                                                                                                              YJL186W OR J0409.
SACCHAROMYCES CEREVISIAE (BAKER'S
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ARTHUR M., MOLINAS C., DEPARDIEU F., COURVALIN P.;
"Characterization of Tn1546, a Tn3-related transposon
glycopeptide resistance by synthesis of depsipeptide p
precursors in Enterococcus faecium BM4147.";
J. BACTERIOL. 175:117-127(1993).
                                                                                                                                                                                                                                                 MEDLINE; 91348521.
ARTHUR M., MOLINAS C., DUTKA-MALEN S., COURVALIN P.;
"Structural relationship between the vancomycin resistance
VanH and 2-hydroxycarboxylic acid dehydrogenases.";
GENE 103:133-134(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
D-SPECIFIC ALPHA-KETO ACID DEHYDROGENASE (EC
RESISTANCE PROTEIN VANH).
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or send an email to license@isb-sib.ch).
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PROSITE; PS00065; D_2_HYDROXYACID_DH_2; 1.

PROSITE; PS00670; D_2_HYDROXYACID_DH_3; 1.

PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.

PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.

PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.

PFAM; PF00389; 2-Hacid_DH; 1.

HSSP; P56297; IDLD.

OXIDOREDUCTASE; NAD; CELL WALL; ANTIBIOTIC OXIDOREDUCTASE; NAD; CELL WALL; 
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SEQUENCE OF 1-32, I
STRAIN-BM4147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HANDWERGER S., PUCCI M.J., VOLK K.J., LIU J., LEE M.S.;

"The cytoplasmic peptidoglycan precursor of vancomycin-resistant enterococcus faecalis terminates in lactate.";

J. BACTERIOL. 174:5982-5984(1992).

-!- FUNCTION: REQUIRED FOR HIGH-LEVEL RESISTANCE TO GLYCOPEPTIDES ANTIBIOTICS. CATALYSES THE REDUCTION OF 2-KETO ACIDS TO 2-D-HYDROXY ACIDS THAT GIVE RISE TO PEPTIDOGLYCAN PRECURSORS THAT TERMINATE IN THE DEPSIPEPTIDE D-ALANINE-1-LACTATE RATHER THAN THE DIPEPTIDE D-ALANINE THUS PREVENTING VANCOMYCIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92394903
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1.250
54.545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL WALL; ANTIBIOTIC RESISTANCE;
31 SUBSTRATE-BINDING (BY SIM:
35795 MW; 0713B1F3 CRC32;
                                                                                                                                                                                                                           ......AlaTyrSerArgSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity:
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E D-ISOMER SPECIFIC 2-HYDROXYACID
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alignment_block:
US-09-030-606-115 x YWBN_BACSU
                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                               Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P39597:
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HYPOTHETICAL 45.7 KD PROTEIN IN EPR-GALK INTERGENIC REGION PRECURSOR.
YWBN OR IPA-29D.
149 CCCATTGGAACTAGTCATTAACCCCATCTCTGAACT...
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X73124; G413953; -. EMBL; Z99123; E1186325; -. PIR; S39684; S39684. SUBTILIST; BG10575; YWBN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Bacillus subtills genome project: cloning and sequencing of the kb region from 325 degrees to 333 degrees."; MOL. MICROBIOL 10:371-384(1993).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRESECAN E., SANTANA M., SCHNEIDER E., RAPOPORT G., DANCHIN A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLASER P., KUNST F., ARNAUD M., COUDART M.P., GONZALES
HULLO M.F., IONESCU M., LUBOCHINSKY B., MARCELINO L., I
                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN; SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                   HisGlnThrTyrValTyrPheAlaAlaLeuAspValThrAlaLysAspLy
                                                                       AAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTC
                                                                                                                                eSerHisGlu.....
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                                                                                                                                                                                                                                                                      Quality:
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                                                                                                                                                               to: YWBN_BACSU
                                                                                                                                                                                                                                                                                                                               29
416 AA;
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                                                                                                                                                                                                                                        60.00
1.429
50.602
                                           416 F
45693 MW;
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                                                                                                                                                                                                                                          Percent
                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL PROTEIN IPA-29D DD543327 CRC32;
                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                       Identity:
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Gaps:
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             GGTAGAAAAACA 195
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6
36.145
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STITE TO THE TRANSPORT OF THE PROPERTY OF THE 
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   CARBOHYD
SEQUENCE
                                                             CARBOHYD
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                                                                                                                                                                                                          DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIYASAKA M., MIYATA T., TANIGUCHI T.;

MUTINE interleukin 2 receptor beta chain: dysregulated gene
expression in lymphoma line EL-4 caused by a promoter insertion.";

PROC. NATL. ACAD. SCI. U.S.A. 87:1806-1810(1990).

-I- FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
MITOGENIC SIGNALS OF IL-2.

-I- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.
                                                                                                                                                                                                                                                                                                                                 CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUKARYOTA; MOTUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P16297;
01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75)
(HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                   CARBOHYD
                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00041; fn3; 1. HSSP; P14784; 1ILN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:96550; ILZRB.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1;
PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: TIFE I PLANTING FRANTLY OF RECEPTORS.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M28052; G309402; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGAAGAGCTAGTCTATCAGCATCTG.....ACAGGTGAA..
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POTENTIAL.
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3A88A84C CRC32;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                          INTERLEUKIN-2 RECEPTOR BETA CHAIN
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MUS.
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lignment	llignment_scores: Quality: 60.00 Ratio: 1.132 Percent Similarity: 45.299	Length: 117 Gaps: 6 Percent Identity: 25.641
11gnmen1 US-09-0:	us-09-030-606-115/rev x IL2B_MOUSE	OUSE
Align seg 1/1	eg 1/1 to: IL2B_MOUSE	from: 1 to: 539
310	-	CATGTAGAGAACCCAAACTAATTTATTAAACAGGATAGAAACAGGCTGTC 261
260		245
296		rSerGlnHisGlyGlyAspLeuGlnLysTrpLeuSerSerProValProL 313
244		GAGAACCATCCAATTCAC 227
313		euSerPhePheSerProSerGlyProAlaProGluIleSerProLeuGlu 329
226		CTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAG 177
330		ValLeuAspGlyAspSerLysAlaValGlnLeuLeuLeuLeuGlnLysAs 346
176		AGATGGGTTAATGACTAGTTCCAATGGGGAAAAAAGCAAGATGGATTC 130
346		pSerAlaproLeuProSer.ProSerGlyHisSerGlnAlaSerCysPhe 362
129		ACAAACCAAGTAATTTTAAACAAAGACACTTTTTTTTTT
363		ThrasnGlnGlyTyrPhePhePheHisLeuProas 374
79		TATACATCACAGTGAAATGTGTAATCCTTGC 49
374		nAlaLeuGluIleGluSerCysGlnValTyrPheThrTyrAspProCys 390

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118.02

21.73

517

559

065473 arabidopsis thaliana ! 076226 trypanosoma brucei

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sp_invertebrate:P91845 - 6.
sp_invertebrate:P91845 - sp_invertebrate:001744 + sp_organelle:033098 - 64.
sp_archea:059203 + 67.
sp_organelle:033098 - 64.
                                                                                                                                                                                                                                                                                                                                                                        ## Sp_invertebrate:020389 + 61.50 125.81 9.93
## Sp_invertebrate:P91904 - 61.50 125.67 9.93
## Sp_invertebrate:P91904 - 61.50 125.67 9.93
## Sp_bacteria:051941 - 61.00 127.74 11.41
## Sp_bacteria:092HF9 - 61.00 127.74 11.41
## Sp_invertebrate:023898 + 60.50 120.33 13.74
## sp_invertebrate:023898 + 60.50 120.33 13.74
## sp_invertebrate:058489 + 60.50 120.33 13.74
## sp_vertebrate:057319 + 60.50 120.30 13.74
## Sp_vertebrate:057319 + 60.50 120.30 13.74
## Sp_pananella:04777 + 60.00 120.82 15.91
## sp_crannella:04777 + 60.00 120.81 15.91
## sp_fungi:092319 + 59.50 128.30 17.79
## Sp_fungi:092319 + 59.50 128.30 17.79
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sp_vertebrate:p79991 - 6
sp_bacteria:068235 + 6
sp_invertebrate:020389 + 6
sp_invertebrate:020389 - 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rodent:Q9Z2E3
sp_bacteria:Q46722
sp_bacteria:P75338
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sp_organelle:079983 -
sp_invertebrate:017945 -
sp_invertebrate:045162 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query length: 366
                                                                                                                                                                                                                      sp_organelle:003101 +
sp_organelle:031904 -
sp_organelle:031922 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database sequences: 201082 Database length: 61543640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_plant:024093
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                                                                                                                                                                                                                                                                                                                                                 sp_invertebrate:016612 +
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-Q-/cgn2_1/USPTO_spool/US09030606/runat_24091999_171617_29869/app_query.fasta.1
-DB-SPTREMBL_10 -QFMT-fastan -SUFFIX-rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOPE-6.000 -DELEXT=7.000 -START=1 -MARTIX-blosumG2
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=escore
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM-stat -USER-US09030606
-NCPU=6 -ICPU=3 -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of: US-09-030-606-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-030-606-115
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71.50 142.46 0.4647 105
68.50 141.15 1.14 506
68.50 141.15 1.14 506
68.50 141.15 1.14 506
- 66.50 137.06 2.12 4
+ 66.00 129.81 2.55 11
- 65.00 128.72 3.45 8
+ 64.50 134.55 3.89 353
64.50 134.41 3.89 353
64.50 134.41 3.89 353
63.50 132.01 5.30 352
63.50 132.01 5.30 352
63.50 128.12 5.41 561
63.50 124.30 5.51 911
63.00 129.35 6.24 421
63.50 120.62 7.56 106
62.50 120.62 7.50 86
62.50 120.62 7.50 106
63.50 120.62 7.50 106
           + 59.50 126.66 17.93

59.50 123.73 18.20

59.50 122.37 18.32

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59.00 133.58 20.10

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462 (017945 caenorhabditis elegans 1972) processes was musculus (mouse). It observed that it is elegans 1112 (054982 mus musculus (mouse). It observed that it is elegans 347 (001744 caenorhabditis elegans 347 (001744 caenorhabditis elegans 347 (001744 caenorhabditis elegans 347 (001744 caenorhabditis elegans 353 (033098 saxifraga ferruginea. ma 354 (054093 medicago truncatula (bar 1946) processes horikoshii. 1 0540722 escherichia colii. hypoth 1976 (1975) processes horikoshii. 1 0540722 escherichia burgdorferi (lypura 19991 xenorhabditis elegans 1055 (197991 xenorhabditis elegans 1051 (19835 borrelia burgdorferi (lypura 19995 schizosaccharomyces pomb 3704 (199104) caenorhabditis elegans 105141 leptospira interrogans. 105141 leptospira borgeterseni 1170 (05315 borrelia burgdorferi (lypura 1991) sarabidopsis thaliana (mc 1992) (05319 gallus gallus (chicken). 1180 (196317) rafrican swine fever visiae (196317) rafrican swine f
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079983 atractylodes
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    Quality:
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sp_invertebrate:076226 -
sp_plant:065481 +
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alignment_block:
US-09-030-606-115/rev x 023424
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DNA CHROMOSOME 4, ESSA I CONTIG FRAGMENT NO. 4.
Arabidopsis thailana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
BEVAN M., STIEKENA W., MURPHY G., WAMBUTT R., POHL T., TERRYN
KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R.,
PUIGDOMENECH P., HATZOPOULOS P., OBERWAIER B., DUESTERHOFT A.
JONES J., PALME K., ANSORGE W., DELSENY M., BANCROFT I., MEWE
SCHUELLER C., CHALWATZIS N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU ARABIDOPSIS SEQUENCING
Submitted (JUN-1997) to tl
EMBL; Z97339; CAB10351.1;
SEQUENCE 1052 AA; 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 ..CTGGGTGAAATGGTTCTGAGAACCATCCAATTCACCTGTCAGATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTCAAGTCACAGACTTTTATGTGACAGATTGGAGCAGGGTTTGTTATG
ThrCys...ProThrLysLeuGlnGlnAsnArgSerLysTyrArgIleGl
                                                                                                laAsnLysIleLysPheValGlyLeu...
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                                                                                                                                               TAAACAAAGACACTTTTTTTTTTTTGCAACACAATATACATCACAGTGAA
                                               ATGTGTAATCCTTGCAAATTGCAAGTTGAAAGAATTAAATTCAGAGGAGG 14
                                                                                                                                                                                                 ......GlnGluGlyCysArgLysAspGlyGluSerAspProArgValA
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Gaps:
Percent Identity: 26
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he EMBL/GenBank/DDBJ databases
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                                                                                                .HisAlaValLysGluLysLys
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yAspLys 407

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seq_documentation_block:
D79983 PRELIMINARY;
AC 079983;
DT 01-NOV-1998 (TrEMBLrel. 08
DT 01-NOV-1998 (TrEMBLrel. 10
DT 01-NAY-1999 (TrEMBLrel. 10
DE MATURASE K.
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    Quality:
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US-09-030-606-115/rev x 078246
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078246 PRELIMINARY;
078246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Phylogenetic analysis of Atractylodes trnK sequence."; Biol. Pharm. Bull. 21:474-478(1998). EMBL; AB008760; BBA332657.1; - PFAM; PF01348; Intron_maturas2; 1. Chloroplast. SEQUENCE 506 AA; 59636 MW; 18F5472D
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Eukaryota; V1ridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; euphyllophytes; Asteridae; euasterids II; Asterales; Asteraceae;
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01-NOV-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                  212
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                                                                                                                                                                                                                                                     TCAGAGATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCAAGATGGATT 131
                                                                                                                                                                                                                                                                                                                  AGATGCTGATAGACTAGCTCTTCAGATGTTTTTC.....TACCAGT 181
                                                                                                                                                         TGCAACACAATATACATCACAG
                                                                                                                                                                                                                                                                                          uAspAlaSerSerLeuHisLeuLeuArgPhePheLeuHisGluTyrHisA 185
                                                                                                                                                                                                                                                                                                                                             TyrProAlaHisLeuGluIleLeuValGlnAlaLeuArgTyrTrpIleGl 168
                                                                                                                                uTyrThrSerHisValCysGlu
                                                                                                                                                                                    .....SerSerSerPheSerLysArgAsnHisArgLeuPhePhePheLe 212
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RRA ROCC OCCUPANT OCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: sp_invertebrate:Q17945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-030-606-115/rev x 079983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: 079983 from: 1
                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Ehahditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                Q17945 PRELIMINARY;
Q17945; Q22858;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1998 (TrEMBLrel. 08,
Q1-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212
DOBSON R.;
Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Pharm. Bull. 21:474-478(1998).
EMBL; AB008762; BAA33659.1; -.
EMBL; AB008758; BAA35655.1; -.
EMBL; AB008759; BAA33656.1; -.
EMBL; AB008761; BAA32658.1; -.
EMBL; AB008761; BAA32658.1; -.
EMBL; AB008761; BAA32658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae;
                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                             T28H10.3
                                                                                                                                                                                                                                                          T28H10.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AGATGCTGATAGACTAGCTCTTCAGATGTTTTTC.....TACCAGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 TyrProAlaHisLeuGluIleLeuValGlnAlaLeuArgTyrTrpIleGl 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast.
SEQUENCE 506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Atractylodes lancea. Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATK.
Atractylodes ovata, Atractylodes chinensis, Atractylodes japonica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trnK sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIRAOKA N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 98297426.
MIZUKAMI H., SHIMIZU R., KOHJYOUMA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Atractylodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phylogenetic analysis of Atractylodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uAspAlaSerSerLeuHisLeuLeuArgPhePheLeuHisGluTyrHisA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uTyrThrSerHisValCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAACACAATATACATCACAG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....SerSerSerPheSerLysArgAsnH1sArgLeuPhePhePheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  snArgAspSerLeuIleThr...SerAsnSerLysLysAla......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGAGATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCAAGATGGATT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATCCAATTCACCTG................
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.50
1.631
56.757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59663 MW;
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      the
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                                                                                                                                                                                                                                                                                       Last sequence update)
      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       586D308D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506
                                                                                                                                                                                                                                                                                                                                                                                                             462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plants based on chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOHDA H.,
                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
5
33.784
                                                                                                                                                                                                                                                                                   update)
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      databases
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                                                                                                                                Caenorhabditis.
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seq_documentation_block:
ID 045162 PRELIMING
AC 045162;
DT 01-JUN-1998 (TrEMBLE
DT 01-JUN-1998 (TREMBLE
DT 01-MAY-1999 (TREMBLE
DE F3784 5 PROTEIN.
GN F3784 5
OS Caenorhabditis elegar
OC Eukaryota; Metazoa; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-030-606-115/rev x Q17945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: sp_invertebrate:045162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1996) to the EMBL; 277653; CAB01126.1; J EMBL; 275551; CAB01126.1; J EMBL; 275551; CAA99935.1; J EMBL; 277653; CAA99935.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]

**SEQUENCE FROM N.A.*

**MEDLINE: 94150718.**

**MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

**WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

**CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

JONES M., KERSHAW J., KIRSTEN J., KOOFTINGRE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., MCHURRAY A., MORTIMORE B., STADEN R.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

**THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAM K., WATERSTON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

**WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

**PARSON S., WEINSON-SPROAT J., WOHLDMAN P.;
                                                                                  O45162 PRELIMINARY; PRT;
045162;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequ
01-MAY-1999 (TrEMBLrel. 10, Last anno
  Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
KERSHAW J.;
                                                                                                                                                                                                                                                                                                                                                                  203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                               ::
1u 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGATGGGTTAATGACTAGTTCCAAT...GGGGAAAAAGCAAGATGGAT 132
                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tH1sLysAsnLysLysTyrSerGlnLeuThrPheTyrLeuGluAlaCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..ValPheValTyrPheThrAspHisGlyAlaValGlyMetIleSerPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                     80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.50
1.330
59.524
        Nematoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 23.810
                                                                                                              Last sequence update)
Last annotation updat
        Secernentea; Rhabditia; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D9A96DC4 CRC32;
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6
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4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
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alignment_block:
US-09-030-606-115 x 045162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: 045162 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
GONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAITER L., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAITER L., JOHNSTON M.,
LIGHTNING J., LOVD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VADUGIN M., WALLSTON R.,
WELNSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M. of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1998) to the EMBL; AF047657; AAC04409.1; PFAM; PF01461; 7tm_4; 1.
                                                                                                                                                                                                                                                                                                                             113, .....AAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCCCAT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HENKHAUS J., WOHLDMANN P., O'BRIEN D.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
301 TCTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTCTG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          154 TGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGAAGA 203
                                                                                                                                                                                                                                                                                                                                                                                      47 etLysSerValLysTrpSerMetPheAsnLeuHisPheTrpSerValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PheLeuAsnHisAlaPheAsn....LeuThrThrCysLeuGlnIlePr 30
                                                                                                                                                                                                                                                                                                                                                                                                                   GCAAAAAAAAAGTGTCTTTGTTT..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTACACATT...TCACTGTGATGTATATTGTGT.....T
                                                                              TCACCC...AGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oIleHisIleLeuGlyAlaTyrCysIleLeuCysLysThrProAspSerM 47
                                                                                                                         yrThrGlyIleSerIleAspValGlnThrTyrLeuIleLeuIleSerTyr
                                                                                                                                                                    GCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATT 253
                                                                                                                                                                                                               aPheAlaGlyPhe...ProLeuGlyVal.....LeuLysT
                                                                                                                                                                                                                                                                                                  LeuAspLeuLysIleThrPheLeuIleSerProPheValLeuPheProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCTCTCCCCCTCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGG
                                      SerAlaLeuGlySerSerIleLeuThrLeuPheGluAsnArgTyrPheLe
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0.985
50.376
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uMetPheAlaLysHisSerSerTrpArgAsnTyrArgHisProPheLeu 140

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seq_documentation_block:

1D 054982 PRELIMINARY;

AC 054982;
AC 054982;

DT 01-JUN-1998 (TrEMBLrel. 06

DT 01-JUN-1999 (TrEMBLrel. 06

DT 01-MAY-1999 (TREMBLORL) 10

DT 01-MAY-1999 (TREMBLORL) 10

DT 01-MAY-1999 (TREMBLORL) 10
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US-09-030-606-115 x P73273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to:
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054982;
01-JUN-1998 (TrEMBLrel. 06, C)
01-JUN-1998 (TrEMBLrel. 06, L)
01-MAY-1999 (TrEMBLrel. 10, L)
POTASSIUM LARGE CONDUCTANCE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
p73273 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D90905; BAA17301.1; --
PFAM; PF00122; E1-E2_ATPase; 1.
PFAM; PF00122; E1-E2_ATPase, 1.
SEQUENCE 972 AA; 106110 MW; 50CB4613 CRC32;
                                                                                                                                                                                       920
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                                                                                                                                                                                                                                                                                                                                                                                               870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T., HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M., TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-AN-1999 (TrEMBLrel. 09, Last annotation update)
CATION-TRANSPORTING P-ATPASE.
                                                                                                                                                                                                                         152
                                                                                                                                                                                                                                                                                                                          886 lIleValAlaCysGlnAspGlyAsnValPheAlaCysArgSerGluArgT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PCC6803;
MEDLINE; 97061201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-PCC6803;
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                                                                                                                                                                                                                                                                                                                                                              <u>6</u>4
                                                                                                                                                                                                                                                                                                                                                                                                                             14 CCTCCTCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACAT
                                                                                                                                                                                                                                                       ATTGGAACT 160
                                                                                                                                                                                                                                                                                         TGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCCC
                                                                                                                                                                                       IleAlaThr 922
                                                                                                                                                                                                                                                                                                                                                                                             ProIleLeuMetAlaIleTyrAlaGlnAlaThrThrMetThrLeuAlaVa
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Ratio:
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62.264
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            Last sequence update)
Last annotation update)
PH-SENSITIVE CHANNEL, S
                                                                                                    PRT;
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                 SUBFAMILY
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alignment_block:
US-09-030-606-115/rev x 054982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_invertebrate:P91845
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Ratio:
Percent Similarity:
        WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN !
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622
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                                                                                                                                                                                                                         Submitted (DEC-1992)
                                                                                                                                                                                                                                         THOMAS
                                                                                                                                                                                                                                                                                       Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
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ZC84.3.
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J. B101. Chem. 0:0-0(1998).
EMBL; AF039213; AAB9742.1; -.
MGD; MGI:1202300; KCNMA3.
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Eukaryota; Metazoa; C
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KCNMA3 OR SLO3
"2.2 Mb of contiguous nucleotide sequence from
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ACAGTGAAATGTGTAATCCT......TGCAAATTGCAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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2.538
50.000
                                                                                                                                                                                                                                                                                     Nematoda; Secernentea; Rhabditia; Rhabditida;
bidea; Rhabditidae; Peloderinae; Caenorhabditi
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Last annotation update)
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Gaps:
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 chromosome III of C.
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                                                                                                                                                                                                                                                                                     Caenorhabditis.
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                                                                                                                                          COULSON A.,
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SPRR
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to:
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET J., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTLMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VADEN M., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 documentation_block:
001744 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans.";
Nature 368:32-38(1994).
EMBL; Z19157; CAA79568.
SEQUENCE 826 AA; 916
                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created) 01-JUL-1997 (TrEMBLrel. 04, Last seq 01-NOV-1998 (TrEMBLrel. 08, Last ann COSMID F35F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386
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                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAGACTAGCTCTTCAGATGTTTTTCTACCAGTTCAGAGATGGGTTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......AACCATCCAATTCACCTGTCAGATGCTG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnCysLeuAsnArgLeuLeuSerAspAlaSerAsnThrMetValLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTTATTAAACAGGATAGAAACAGGCTGTCTGGGTGAAATGGTTCTGAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTAGTTCCAATGGGGAAAAAGCAAGATGGATTCACAAACCAAGTAATTT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....AGTGAAATGTGTAATCCTTGCAAATTGCAAGTTGAAAG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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1.226
51.456
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Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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alignment_scores:
Quality:
Ratio:
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SO SET DIT DE LEG
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US-09-030-606-115 x 001744
                                                                                                                                         seq_name: sp_organelle:Q33098
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                                  Q33098 PRELIMINARY;
Q33098;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-JAN-1999 (TrEMBLrel. 0
MATURASE (FRAGMENT).
                                                                                                                _documentation_block:
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[2]
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      MATK.
Saxifraga ferruginea
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Gaps: 6
Percent Identity: 24.444
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                                                sequence update)
annotation update)
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Chloroplast

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seq_documentation_block:
ID 059203
AC 059203;
DT 01-AUG-1998 (TrEMBLTE
DT 01-AUG-1999 (TrEMBLTE
DT 01-ANG-1999 (TrEMBLTE
DE 136AA LONG HYPOTHETIC
GN PH1534.
OC AICHAGA: EULYARCHAGOT
RN SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE; 98344137.
RA KAWARABAYASI Y. SAWA
RA KAWARABAYASI Y. SAWA
RA KAWARABAYASI Y. TANAKA
RA KAWARABAYASI Y. TANAKA
RA KAWARABAYASI T. TANAKA
RA KAWARABAYASI T. TANAKA
RA KAWARABAYASI T. TANAKA
RA KIKUCHI H.;
RT DNA RGS 5:55-76(1998)
DNA RGS 5:55-76(1998)
EMBL; APOOOOOG; BAA3(1998)
DR EMBL; APOOOOOG; BAA3(1998)
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US-09-030-606-115/rev x Q33098
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Percent Similarity:
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MENDEL; 5094;
Chloroplast.
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                                                                                                                 MEDLINE; 98344137.

KAMARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., OHEUKU Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHEUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
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01-AUG-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
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                                          "Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.", DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217
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JOHNSON L.A., SOLTIS D.E.,
Ann. Mot. Gard. 0:0-0(0).
EMBL; L34141; AAA84602.1; -.
MENDEL; 5094; SAXfe;ycf14;1.
                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Thermococcales;
                                                                                                                                                                                                                                                                                                                      Pyrococcus horikoshii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                            BAA30644.1;
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52.113
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        15267 MW;
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07, Last sequence update)
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Gaps: 3
Percent Identity: 30.986
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      5F920399 CRC32;
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US-09-030-606-115/rev x Q31804
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Quality:
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Quality:
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Percent Similarity:
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Ann. Mo. Bot. Gard. 0:0-0(0).
EMBL; L34114; AAB03515.1; -.
MENDEL; 5033; ASTja;ycf14;1.
Chloroplast.
NON_TER 352 352
                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Saxifragales; Saxifragaceae; Astilbe.
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                                                                                        169 sAspAlaSerSerLeuHisLeuLeuArgPhePhePheTyrGluTyrGlnA
                                                                                                                                                                                                                                                                                                                                                             238 CATCCAATTCACCTG.....TC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
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                                                                                                                                              AGATGCTGATAGACTA...GCTCTTCAGATGTTTTTCTACCAGTTCAGA. 176
....GATGGGTTAATGACTAGTTCCAATGGGGAAAAAGCAAGATGGATT
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Gaps: 2
Percent Identity: 31.250
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Last sequence update)
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131
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seq_documentation_block:
ID 024093
AC 024093
AC 024093
AC 024093
AC 01-JAN-1998 (TrEMBLIZE
DT 01-MAY-1999 (TREMBLIZE
DT 01-MAY-1999 (TREMBLIZE
DT 01-MAY-1999 (TREMBLIZE
DE L-ASCORBATE OXIDASE P
GN MEDICAGO truncatula (
CC Eukaryota; Viridiplan
OC Eukaryota; Viridiplan
OC Eukaryota; Viridiplan
OC Core eudicots; Rosida
CC Medicago.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-CV. JEMALONG J
RX GAMAS P., DE CARVALHO
RT "Use of a subtractive
RT TURCATULA genes indu
MAL Plant Microbe In
RN [2]
RP SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
RC GAMAS P.;
SUBMITTE: PS00079; MUL
DR PROSITE: PS00079; MUL
DR PROSITE: PS00079; MUL
STRAIN-CV SEQUENCE STRAIN
DR PROSITE: PS00079; MUL
DR PROSITE: PS00079; MUL
STRAIN-CC SEQUENCE S69 AA; 6
                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-030-606-115/rev x 024093
                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality:
seq_name: sp_rodent:Q922E3
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                                                                                                                                                                                                                                                                                          Align seg 1/1 to: 024093 from: 1
                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O24093 PRELIMINARY; PRT; 569 AA.
024093;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
L-ASCORBATE OXIDASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1997) to the EMBL/GenBank/DDBJ
EMBL; Y15295; CAA75577.1; -
PFAM; PF00394; Cu-oxidase; 2.
PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMAS P., DE CARVALHO NIEBEL F., LESCURE N., CULLIMORE J.; "Use of a subtractive hybridization approach to identify n truncatula genes induced during root nodule development."; Mol. Plant Microbe Interact. 9:233-242(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. JEMALONG J5; TISSUE-ROOT NODULE;
MEDLINE; 96212994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula (Barrel medic).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
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                                        lyArgPheArgProGlyVal 491
                                                                                 ACCAGTTCAGAGATGGGTTA 167
                                                                                                                        sProTrpHisLeuHisGlyHisAspPheTrpValLeuGlyTyrGlyGluG
                                                                                                                                                                TCCAATTCACCTGTCAGATGCTGATAGACTAGCTCTTCAGATGTTTTTCT
                                                                                                                                                                                                         IleLeuGlnAsnAlaAsnGlnLeuAsnGly...AsnGlySerGluIleHi
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2.646
60.000
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569
63973
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Identity: 45
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seq_documentation_block:
ID Q922E3
AC Q922E3;
AC Q022E3;
AC Q022E3;
AC Eutheria;
AC
   RR CCC E DI DI AG
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ID Q46722 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-030-606-115 x Q9Z2E3
                                                                                                                                                                                                                                                                                                                                                                               seq_name: sp_bacteria:Q46722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
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WANG X.Z., HARDING H.P., ZHANG Y., JC
"Cloning of mammalian Irel reveals a
responses.";
EMBO J. 17:5708-5717(1998).
EMBL; AR071777; AAC64400.1;
SEQUENCE 911 AA; 101355 MW; 57240
                                                    Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 rLeuAspThrGlnLeuLeuMetThrLeuTyrValGlyLysGluGluAlaG
                                                                                                                                              HYPOTHETICAL 47.2 KD
                                                                                                                                                                                                                                                                   Q46722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 TCTCTACATGCATAACAAACCCTGCTCCAATCTGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 ThrAlaValArgTyrProSerGlySerValAlaLeuProSerGlnTrpLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 Arg.......GlyLeuThrLeuAlaProMetAspGlyProThrThrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 lyPheTyrValSerLysAlaLeuValHisAlaGlyValAlaLeuValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 TCTTT...GTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 IleArgLeuProAlaSerSerTyrGlnAspThrAlaThrGlnPheSerSe
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 CATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uLeuIleGlyTyrHisGlu.ProProProValLeuHis 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTCACCCAGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pGluValThrLeuGln...ValSerGlyGluArgGluGlySerPro.Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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Gaps:
Percent Identity:
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                                                                                                                                                                                                                                       Created)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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AA972883 455 bp mRNA EST 07-J1 000249(07:\$1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1577820 3', mRNA sequence. AA972883 93148063 4A972883.1 GI:3148063
EST sapiens cDNA
07-JUL-1998 clone

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1 (bases 1 to 455)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA Tumor Gene Index Unpublished (1997)
On Jan 9, 1998 this sequence version replaced gi:937931.
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Email: Robert 7
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 633 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                      /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.

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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:
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                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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nj43e11.s1 NCI_CGAP_Pr9
sequence.
AA809587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
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On Jan 19, 1998 this sequence version replaced
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                                                       /tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells, cDNA made by oligo-dr
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Krizman, NIH."
96 c 68 g 151 t
                                                                                                                                                                                                             /organism-"Homo sapiens"
/db_xref="taxon:9606"
/map-"90209; 2: 2911.2-2p13.1"
/clone="IMAGE:995276"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Homo sapiens cDNA clone IMAGE:995276,
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Length 435;
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RESULT 4
AA813266/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a)44g03.sl Soares_testis_NHT mRNA sequence.
                                                                                                            Insert Length: 982 Std Error: 0.00
Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 503.
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1 (bases 1 to 599)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                             Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                       CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CCGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1393204"
/clone_11b="Soares_testis_NHT"
                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            1995 this sequence version replaced gi:775316
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                                        (197)

(Jases 1 to 490)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-Merck EST Project 1997

Unpublished (1997)

On Sep 12, 1905
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                                                                                                                                                                                                                                                                  zv54b10.s1
3' similar
Contact: Wilson Washington Unive
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              EST
                                                                                                                                                                                                                          g2142138
AA437224.1 GI:2142138
                                                                                                                                                                                                                                                    3′ similar
AA437224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(primer [5']
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       University
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Pred. No. 2.6e-71;
        School of Medicine
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This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Seq primer: -41ml3 fwd. ET from Amersham High quality sequence.stop: 363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
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/db_xref="GDB:5978049"
/db_xref="taxon:9606"
/map="6 p23-p22; 949D05; 2;
/clone="IMAGE:757435"
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Pred. No. 7.7e-71;
0; Mismatches 0;
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Homo sapiens cDNA clone
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GCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCCCTG
                                                                                      CTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATTTCACCCAGACA 264
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                                          GCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCCTG 324
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1 (bases 1 to 423)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA)
Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (301) 496-1550
Email: Robert_Strann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. B:
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.4%; Score 342; DB 50; ilarity 100.0%; Pred. No. 1.5e-68; Conservative 0; Mismatches 0;
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/map="19p12-p13.1"
/clone="IMAGE:2248757"
/clone=11b="NCI_CGAP_Pr28"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-*Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_PT22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 66.c 83 g 124 t
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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similar to
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Seq primer: -41ml3 fwd. EP from Amersham
High quality sequence stop: 368.
Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 419)
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                          Similarity
                                                                                                                                                                                                                         141
                                                                                        Conservative
                                                                                                                                                                                                              /dev_stage="45 years old"
//dev_stage="45 years old"
//lab_host="DHIOB"
//lab_host="PHIOB"
//note="Vector: pAMPIO; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMPIO by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
41 a 68 c 79 g 131 t
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/clone_lib="NCI_CGAP_Pr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 NCI_CGAP_Pr2
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Pred. No. 5.6e-62;
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Homo sapiens cDNA clone IMAGE:1010092
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                                                                                                                                                                                                                                                                                                                    Seq |
High
                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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On Dec 30, 1996 th
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nr28d08.rl NCI_CGAP_Pr3
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National Cancer Institute, Cancer Genome Anat
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n quality sequence stop: 387.
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Location/Qualifiers
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     5,000-10,000 microdissected cells histologically determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life
                                                                                                         /dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAmP10; Site_1: Not1; Site_2: EcoRI;
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1169295"
                                                                                                                                                                                                /clone_lib="NCI_CGAP_Pr3"
/sex="Male"
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AI672753
g4852484
AI672753.1
                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI672753
we58dl0.xl
                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
On May 18, 1998 th
                                                                                                                                                            IMAGE Consortium (info@image.llnl.gov) Seq primer: -40UP from Gibco High quality sequence stop: 362.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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directionally c
David Krizman."
a 80 c 6
                                                       /map="952F05; 14; 14q23.1-14q24.1; MMU16C3-C4 region"
   /clone="IMAGE:2345299"
/clone_lib="Soares_thymus_NHFTh"
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/db_xref="taxon:9606"
                                                                                                                                           Location/Qualifiers
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Pred. No. 5e-60;
); Mismatches
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18-MAY-1999 element;,

Project (CGAP),

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RESULT 10
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SOURCE
                                                                                                                                                                                                                             JOURNAL COMMENT
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TITLE
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                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Grey Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA533772 445 bp n
nj93c05.s1 NCI_CGAP_Prl1
mRNA sequence.
AA533772
                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On May 8, 1995 this
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 445)
                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                              www-bio.llnl.gov/bbrp/image/image.html
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613
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Std
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Error:
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AA531606/c
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          Tel: (301) 496-1550
Email: Robert Strausberg, Ph.D.
Temail: Robert Strausberg, Ph.D.
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                                                                               Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 423)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA)
                                                                                                                                                                                                                                                                                                                                        AA531606 423 bp n
nj65e04.s1 NCI_CGAP_Pr10
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Robert_Strausberg@nih.gov
Procurement: W. Marston L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1000040"
/clone_1ib="NCI_CGAP_Pr11"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="normal prostatic epithelial cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                  replaced g1:1395365
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IMAGE:997374,
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Marston Linehan, M.D.,

Rodrigo

F. Chuaqui,

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REFERENCE
AUTHORS
                                                                  SOURCE
ORGANISM
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AA493522
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ORIGIN
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317; Conserv
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
                                                                                                                                                                              AA493522 403 bp
ng75f05.sl NCI_CGAP_Pr6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="invasive prostate tumor"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                 GI:2223363
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97.8%;
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Homo
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Query Match
Best Local
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                                                                                                                                                                                                                                                                           AACTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300;
AA650104 339 bp
ns92f11.s1 NCI_CGAP_Pr3
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Tissue Procurement: David G. Bostwick, M.D., Rodr
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-GCAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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Unpublished (1997)
On Jun 18, 1996 this sequence version replaced gi:1366614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pamp10; mRNA made from prostatic intraepithelial neoplasia (low-grade), cDNA made by oligo-dr prining. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:940641"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Pr6"
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99.3%;
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Pred. No. 2.7e-56;
0; Mismatches 0;
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Homo
sapiens cDNA clone IMAGE:1191117,
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                      13-NOV-1997
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KEYWORDS
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Best Local :
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  182 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTT
                                                                    122 TGGTTTGTGAATCCATCTTGCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAA 181
                                                                                                                                    Local
                                                                                                                                                          51 CTCTGTCTCCCCTCCTCTGAATGTAATTCTTTCAACTTGCAATTTGCAAGGATTACAC 110
                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                       CTCTTTCTCCCCCCCCCCCTCAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACAC 61
                                               TGGTTTGTGAATCCATCTTGCTTTTTCCCCCATTGGAACTAGTCATTAACCCATCTCTGAA
                                                                                                                                                                                                                                                                                                                       286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 339)
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National Cancer Institute, Cancer Genome Anatomy
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AA650104.1 GI:2577432
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//dev_stage="45 years old"
//lab_host="PuH10B"
//nbc="vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected cells
histologically-determined to be fully malignant prostate
cancer cells. Double-stranded cDNA was ligated to EcoRI
adaptors, 5 cycles of PCR applied to the CDNA with an
adaptors-pecific primer, and the resulting PCR product
subcloned into pAMP10 by the UDG-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
David Krizman."

94 a 72 c 57 g 116 t
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/db_xref-"taxon:9606"
/mapp-"17q21: between D17S1321 and D17S1325"
/clone-"IMAGE:1191117"
/clone-1ib-"NCI_CGAP_Pr3"
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Pred. No. 2e-55;
O; Mismatches 3;
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  134 CCATCTTGCTTTTTCCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAA 193
                                                                                                                                   Local Similarity
nes 292; Conserv
                                                                                     75 GTATATTGTGTTGC-AAAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAAT 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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On Dec 20, 1995 this sequence version replaced
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AI669511.1
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                     132
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                              /note-"organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 986759, l101192-1101599, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "as 61 c 74 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2312773"
/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'lab_host-"DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                      76.8%; Score 281; DB 50; Length 377; 99.7%; Pred. No. 1e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCACCCAGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCAT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATT 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 374)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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W47380.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq_primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
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W47380
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                      131
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              double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fattina Bonaldo."
                                                                                                                                                                                                                               /Clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/tissue_type="senescent fibroblast"
/lab_host="DH108 (ampicillin resistant)"
/lab_host="PT973D (pharmacia) with a modified
/note="Vector: pT773D (pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; lst strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                     /clone="IMAGE: 324741"
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Query Match

76.5%;

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                                                                CACCCAGACAGCCTGTTTCTATCCTGTTTTAATAAATTAGTTTGGGTTCTCTACATGCATA 314
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Search completed: September 28, 1999, 11:29:30 Job time: 1851 sec

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4 41.8 11.4 119707 35 ACCO77180
5 41.8 11.4 119707 35 ACCO77180 ACCO77180 ACCO77180 Drosophil
5 41.8 11.1 4 77685 37 ACCO5444
6 40.4 11.0 262336 34 ACCO6798
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8 40.4 11.0 2005509 34 ACCO67910 ACCO6730 Caenorhabd 39.8 10.6 190500 34 ACCO6710 ACCO67310 ACCO
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ALIGNMENTS

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SHGC-57295 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G37241
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VERSION G37241.1 G1:2996892
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SOURCE
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE
JOURNAL
COMMENT
CONTACT: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259689
Email: myers@shgc.stanford.edu
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
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Sciavolino,P.J., Abrams,E.W., Yang,L., Austenberg,L.P., Shen,M.M. and Abate-Shen,C.
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Submitted (04 FEB-1997) CABM,
Piscataway, NJ 00854, USA
Location/Qualifiers
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                                               Bevan, M., Murphy, G., Drost, L., Hall, C., Hudson, S., Bancroft, I., Mewes, H.W., Mayer, K. and Schueller, C.
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complement(join(43374424,44994645,47395174, 59456138,62836882,83918639,87429232)) /gene="similarity to downy mildew resistance protein RPP5, Arabidopsis thaliana, PATCHX:G2109275" /codon_start=1 /product="downy mildew resistance-like protein" /protein_id="cAA16600.1" /protein_id="cAA16600.1" /protein_id="cAA16600.1" /db_xref="plD:9287646" /db_xref="plD:9287646" /db_xref="gl:2827646" /db_xref="gl:2827646" /db_xref="gl:2827646" /db_xref="gl:2827646" /db_xref="gl:2827646" /db_xref="gl:2827646" /db_xref="gl:2827646" /db_xref="gl:2827646" /db_xref="gl:2827646" /db_xref="plD:9287646" /db_xref="plD	/gene="fl8f4.20" complement(43374424) /gene="fl8f4.20" /number=1	/mumber=4 4337. 9232	•	complement(26942855) /gene="F18F4.10" /number=3	complement(4712693) /gene="F18F4.10"	/udiber=r complement(322470) /gene="r18F4.10" /number=7	/number=1 complement(252321) /gene="F18F4.10"	complement(141251) complement(141251) /gene_*F18F4.10"	/db_xref="G1:827645" /db_xref="G1:827645" /db_xref="SPTREMBL:049418" /translation="MAKLLCSYLFICMFYLSGFLVFSSAKQLKTCTSVIKLGHPCDIE /CLNECFRYVNTGFATCRGDKYSQLCTCTPNPNVALDELVKIKELVDKGGLVTIPISY KIFTSNVGTLKOFFGTMENGKSGXMAVAVVNVMTITNVENTIOFFGTATCFGT	<pre>/product="hypothetical protein" /protein_id="CAA16599.1" /db_xref="PID:e1248720" /db xref="PID:e2827645"</pre>	<pre>/gene= rior4.10 /note="protein sequence is in conflict with the conceptual translation." /codon_start=1</pre>	/gene="risk4.10" complement(join(138251,322470,26942855,32193270))	/chromosome="4" 138. 3270	/organism="Arabidopsis thaliana" /variety="Columbia" /db_xref="taxon:3702"	Direct Submission Submitted (03-FEB-1998) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Project Coordinator: Mike Bevan, Molecular-Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk Location/Qualifiers 1. 9366
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//db_xref="gIT:eJ276 14707 15942 /gene="F1874.40" /number=1 14707 15942 /gene="F1874.40" 14707 15942 /gene="F1874.40" complement(6283. /gene="F18F4.20" /number=5 RVNTDDVKNFKGKFGSCFIETVQRQSPKEEPMAERWVNSVKSISSKTGFTSEVHRIDS YLVDAIVRDVKRQLPYVPTKEKELPIETEIFFALVLAGICNETALGINDTSSYKTPQ WEVVFINHGESDQSDGFIRHVERALDEGFUNFIDSDERRGRGMEHIFRAIDNSUNAL VIFSDRYTASELCLHEAVRIYDBRREGKLVLIPVFYRVSEDDVNMFNGRFGESFLETL TIQGFRDHPFAEHMMRNVNF1CTDTGFTSADYSSNDTSLVEETVRAIKRRLQGKKLPR RVQDEKLPSPLDMFMFKQPNAQEGLDVFSILQMLVAVLSLVVIRKTFRLILS" COMplement(4425. 4498) /gene="F18F4.20" complement(6883. /gene="F18F4.20" complement(6139. /gene="F18F4.20" complement(4739. /gene="F18F4.20" complement(4646. .4738) /gene="F18F4.20" complement(4499. .4645) /gene="F18F4.20" complement(8742. .9232) /gene="F18F4.20" complement(8640. /gene="F18F4.20" complement(8391. /gene="f18f4.20" complement(5945./gene="F18F4.20" complement(5175. /gene="F18F4.20" /gene="F18F4.30" 12070. .13365 /gene="F18F4.30" /note="similarity to W20DMY30S" /number=5 /number-3 'number-12070. .13365 /gene="F18F4.30" /number=6 /number=4 /number=4 /number=3 /number=2 /number=2 number-2070. .13365 .6138) .5944) .8741) . 8639) .8390) .6882) .6282) .5174)

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                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                 TTTTTCCCCATTGGAACTAGTCATTA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTAAATTCTTTCTAATTTTATTGTACACTTATTATACATCGAATCTATATGTTTAATG 3713
Eukaryota; Metazoá; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 119707)

Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L.,
                                                                                                                                                                                                                   ACUU/180 119707 bp DNA HTG 14-MAY-1999
Drosophila melanogaster chromosome 2 clone BACR01G10 (D539) RPCI-98
01.G.10 map 360-36D strain y2; cn bw sp, WORKING DRAFT SEQUENCE, 21
                                                                                                               Drosophila melanogaster
                                                                                                                                             AC007180.6 GI:4827280
HTG: HTGS_PHASE1.
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                                                                                                                                                                                                        unordered pieces.
                                                                                                                                 fruit fly.
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/brotein_id="CAA16603.1"
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/db_xref="plD:e327649"
/db_xref="GI:2827649"
/db_xref="GI:2827649"
/db_xref="SPTREMBL:049422"
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AILAHSLFTQPILAQIDTYPQADQSQLQHEWTVLLVFQFCYIIFLFAFSLLSTAAVVF
TVASLYTGKPVSFSSTMSAIPLYLKRLFITFLAVSLLMLAYNTVFLLFLVTLIVAVDL
QNVVLAVFSLVVIFYLFLVVHVYMTALMHLASVVSVLEPIYGLAAMKKSYELLKGKTL
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DKSALHDHLGGYLGEYVPLKSNIQMENFEV"
18489. .19271
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LQVPGDIFWKYNGLLEYGGKIAILNYTKVDIEGVMELWVVEDEEKNLWSSKILVVNPL
QLQMVNSIISLTVLGTTRNGEVILVPGPEDKTVFNILLYDLQKNHIRKIEIKGGPDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRLPAKSLMRFKSVSKLWSSLICSRNFTNRLLKLSSPPRLFMCLSSSDNSHLKTVLLS
LSSPPDSDITMSSSVIDQDLTMPGMKGYQISHVFRGLMCLVKKSSAQIYNTTTRQLVV
LPDIEESTILAEEHKSKKIMYHIGHDPVYDQYKVVCIVSRASDEVEEYTFLSEHWVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"similarity to p48 eggshell protein Schiptosoma manson1, PATCHX:G454844"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:049421"
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Pred. No. 0.
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Unpublished

2 (bases 1 to 119707)

2 (bases 1 to 119707)

Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chiker, S.E., Agbayani, A., Chavez, C., Chew, M., Ciestolka, L., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciestolka, L., Butenhoff, C. M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Doyle, C.M., Farfan, D.E., Galle, R., Karra, K., Kearney, L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Hoskins, R.A., Moshrefi, M., Nixon, K., Dacleb, J.M., Park, S., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequelra, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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submitted (29-MAR-1999) Drosophila Genome Center, Lawrence Berkeley, Laboratory, MS 64-121, Berkeley, CA 94720, USA On May 14, 1999 this sequence version replaced gi:4764154. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the collowing cutoffs: length >= 400 bases, phrap computed error

NOTE: This is a 'working draft' sequence. It currently consists of 21 contlys. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

gap of unknown length contig of 725 bp in length gap of unknown length contig of 1275 bp in length gap of unknown length contig of 676 bp in length gap of unknown length contig of 676 bp in length gap of unknown length contig of 963 bp in length contig of 1042 bp in length unknown length of 1423 bp in length n length
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                                                                                                                                                                                                                                                                           Celniker.S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Boyle, C. M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Humasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Punch, E., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Sequencing of Drosophila chromosome 2R, region 36D3-36D3
                                          Unpublished (1998)

2 (bases 1 to 77685)

2 (bases 1 to 77685)

2 (bases 1 to 77685)

2 (clniker,S.E., George,R.A., Galle,R., Svirskas,R.R., Hoskins,R.A., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Chew,M., Karra,K., Kearney,L., Kim,S.H., Lee,B., Lomotan,M.A., Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R., Lomotan,M.A., Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R., Piciffer,B., Punch,E., Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and Kimmel,B.E.
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1 (bases 1 to 77685)
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Submitted (14-AUG-1998) Drosophila Genome Center,
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/Clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBACe3.6"
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/db_xref="taxon:7227"
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  Lawrence Berkeley
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On Mar 1, 199 this sequence version replaced gi:4263152.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Pl library location: 67-43.
                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhab
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                                                                                                                                                                                                                    Direct Submission
Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                        2 (bases 1 to 262336)
Waterston, R.H.
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Waterston, R.H.
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Caenorhabditis elegans.
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Similarity 55.0%;
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/Clone_lib="p1 library, partial Sau3A in pAd10sacBII"
/clone="p1 DS06379 (D358)"
/clone="p1 DS06379 (D358)"
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/db_xref="taxon:7227"
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Rhabditidae; Peloderinae; Caenorhabditi
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Matches 98
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                                                AC006798.2 GI:4309785
HTG: HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 207370)
Materston,R.H.
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l Similarity 50.5%;
98; Conservative
                The sequence of Caehorhabditis elegans clone Unpublished
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1. .262336
/organism="Caemorhabditis elegans"
/db_xref="taxon:6239"
/clone="Y48G8"
/ 46255 c 46078 g 84102 t 2411
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13934: gap of unknown length
16026: contig of 2092 bp in length
16035: gap of unknown length
16135: gap of unknown length
16143: gap of unknown length
161281: contig of 59419 bp in length
161281: contig of 79818 bp in length
163945: contig of 2655 bp in length
163954: gap of unknown length
163954: gap of unknown length
167128: contig of 3174 bp in length
167128: contig of 3174 bp in length
167137: gap of unknown length
167137: gap of unknown length
202845: contig of 3174 bp in length
202845: contig of 3174 bp in length
205093: gap of unknown length
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209517: contig of 4230 bp in length
209526: gap of unknown length
209526: gap of unknown length
221802: gap of unknown length
221802: gap of unknown length
231649: gap of unknown length
231641: contig of 3553 bp in length
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231641: contig of 35687 bp in length
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Pred. No. 2;
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Direct Submission

Submitted (23-FEB-1999) Genome Sequencing Center, Washing University School of Medicine, 4444 Forest Park Parkway,
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Query Match Best Local S Matches 98

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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; S.
Rhabditina; Rhabditoidea; Rhabd
1 (bases 1 to 200509)
Waterston, R. H.
                                                                                                                                                                                Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Mar 1, 1999 this sequence version replaced gi:4263438.
* NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                 unordered pieces
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., Rifken, J., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Watson, J., Matson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
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AF043701
This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by sequence from more than one subclone
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-JAN-1998) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 40479)
Wamsley,P. and Kramer,J.
The sequence of C. elegans cosmid K12C11
Unpublished (1998)
3 (bases 1 to 40479)
Waterston,R.
                                                                                                                                                           NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditina; Rhabditoidea; Rhabditida; Peloderinae; Caenorhabditis. 1 (bases 1 to 40479)
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Caenorhabditis elegans
                                                                                                                                            neighboring submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submission
                                                                                                                                                                                                                                                                                                     Department of Genetics, Washing St. Louis, wo 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CBIO IRO, England
                                                                                                                                                                                                                                                                                  e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center
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                                                problems,
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gene

NEIGHBORING COSMID INFORMATION:

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actual
                                                            The 5'
cosmid is Y48G8A;3' cosmid is GAPlarm_65, 200 bp overlapstart of this cosmid is at base position 1 of CELK12C11; end is at 40479 of CELK12C11
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FEATURES
source
                                             the
                                                                     Coding
                                             program
                                           sequences below are predicted from computer analysis, using ogram Genefinder(P. Green and L. Hillier, ms in preparation)
                     Location/Qualifiers
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gene /translation="KNGSKALKFSEISIIFVKIEAAELCNRKNCGKADFFSQNCPTGAITIEPGCYFIDFLLNEALADPKKSEFLVKSEIDKYRGSGGVRIEDDVIIRASGNENLSDLPRTVEEIENEMASGGEWTEKVIESRVSDFLSK" complement(1200. .1581) /gene="K12C11.2" /note-"contains similarity to the M24B family of peptidases; coded for by C. elegans cDNA yk169c2.3; coded for by C. elegans cDNA yk135e10.3" /protein_id="AAB97576.1" /db_xref="PID:g2804467" /db_xref="GI:2804467" join(<356. .484,648. .929) /gene="K12C11.1" /strain="Bristol N2" /codon_start=1 /gene="K12C11.1" /db_xref="taxon:6239" /chromosome="I" organism="Caenorhabditis" one-"K12C11" elegans"

Coded for by C. elegans cDNA yk118b3.3; coded for by C. elegans cDNA yk18b3.3; coded for by C. elegans cDNA yk18b3.3; coded for by C. elegans cDNA yk18b3.3; coded for by C. elegans cDNA yk14b3.3; coded for by C. elegans cDNA yk114b3.3; coded for by C. elegans cDNA yk114b3.3; coded for by C. elegans cDNA yk118b3.5; coded for by C. elegans cDNA yk118b3.5; coded for by C. elegans cDNA yk114b3.5; coded for by C. elegans cDNA yk114b3.5; coded for by C. elegans cDNA yk114b3.5; coded for by C. elegans cDNA yk12b2.5; coded for by C. elegans cDNA yk12b3.5; coded for by C. elegans cDNA yk12b3.5; coded for by C. elegans cDNA yk13b5.5; coded for by C. elegans cDNA yk13b5.5. complement(join(1200. .1308,1359. .1459,1516.
/gene="K12C11.2" 'codon_start-1

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gene

CDS

/translation="MADDAAQAGDNAEYIKIKVVGQDSNEVHFRVKYGTSMAKLKKSY ADRTGVAVNSLRFLFDGRRINDDTPKTLEMEDDDVIEVYQEQLGGF" complement(2574. .6889) /gene="K12C11.3" complement(join(2574. .2653,2665. .2720,2914. .3008, complement(join(2574. .2653,2665. .2720,2914. .3008, 3289. .3479,4202. .4347,4912. .5029,5168. .5270,5985. .6079 6126. .6288,6769. .6889)) /gene="K12C11.3" /evidence=not_experimental
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/db_xref="PID:92804469" codon_start=1/ .6075

QAMYHFWQTLLAFILMNIYMTENKKMKISGPPEMHMWFHTKTQDTVLFKTWNVTDTPT MVWVCCIIVVAGILLELIKFLRWKIEKWHKNRDELVSRSYISRLFSPIHIGQTILFMV QLSESYILMLLFMTESVWLGIAVVVGLGIAMMMDMWQMYFHFRIQEPILFRQWKPTDT /db_xref="GI:2804469"
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/translation="MSLNTSTMAPMGKTTKMWGWYHVELNDVILFENWKVQDMTTWIW
SCFVVGFAGFILFENKKLFWAARHVV TGYVFSCISLFFIAFCLELLKFGRQRMTRTVKEKLAVDCCCSTPEGIWEIPEEPEPSP RGKLASLAPRFYLFFFFFEFLEEKLKIRHAIGYFFVGPLMTVKEVENTGNCCS"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTGTGTTGCAAAAAAAAAAGTGTCTTTGTTAAAATTACTTGGTTTGTGAATCCATC 138
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D87009
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LCRILVELGRCDARDALYRTVPLYVFAPLEDQFLLETNDSGVVSSCHSSSEHNPINIT
25918. .26212
/note="C. elegans telomere-like hexamer repeat"
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/db_xref="GI:2804470"
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/gene="K12C11.4"
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        GI:2114252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawasaki,K., Minoshima,S., Nakato,E., Schmeits,J.L., Wang,J. and Shimizu,N. One-megabase sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimizu, N
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                          'gene="V3-1P"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'clone="288A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="human pre-pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell_line="FLEB14-14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="QPVLTQPPSSSASPGESARLTCTLPSDINVGSYNIYWYQQKPGS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="V4-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="V1-12P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRYLLYYYSDSDKGQGSGVPSRFSGSKDASANTGILLISGLQSEDEADYYCMIWPSN
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                                                                                      .70486)
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VERSION
KEYWORDS
SOURCE
                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                       CEK08E3
                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 71; Conserv
                            TITLE
                                                                                                                               ORGANISM
  JOURNAL
                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51580 TITCTTTCCTTTGCTCTGAAAGTTCTTCTTTTATCTGACAATTTAATACCCACCTGTAAT 51521
                                                                                                                                                                                                                                                                                                                                                                                          51460 ATT 51458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 TTTCTCTCCCCTCCTCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITCITIGACTGATAGGATGITGGAGAATATATAAAATITITAATITCITAATITTAATITTAGTITT 51461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCACTGTGATGTATATTGTGTTGCAAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGG 124
                                                             Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 39565)
Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail
                                                                                                                                                                                                                                                           Caenorhabditis
                                                                                                                                                                                                                                                                                 CEK08E3
                                              McMurray,A.
                                                                                                                                                                                                                 g3643297
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                        Submission
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1 22463 c 22062 g 28666 t
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VCQVCHYRSSVFADVETHFRTCHENTKNLLCLFCLKLFKTAIPYMNHCWRHSRRRVLQ
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QPGSVDVASITVSTSDSEPSLPRSKSKISKKSH"
complement(95093. .96717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENPIVLLSDFYYGQHKGEGQPEQKTHTTFKCLSCVKVLKNVKFMNHVKHHLEFEKORN
DSWENHTTCQHCHRQFPTPFQLQCHIENVHTAQEPSTVCKICELSFETDQVLLQHMKD
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NVHTSLSHVQNGAPFPAAFPKONIHFKPINTNLDRENELAKTDILSLTSQNKTFDPKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"putative"
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/codon_start=3
                                                                                                                                                                                                                                                                              39565 bp
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                                                                                                                                                                                                                                                      elegans
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Pred. No. 3.2;
                                                                                                                                                                                                                                                  cosmid K08E3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Length 104386;
                                                                                                                                                                                                                                                                              23-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bin/display/db=wormacesclass=Sequence &object=K08E3
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone K08E3. The true right end of clone W06F12 is at 467 in this sequence. The start of this sequence (1. .105) overlaps with the end of sequence Z83244.

The end of this sequence (39514. .39565) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94150718
On Sep 23, 1998 this sequence version replaced gi:3294143.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans
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2  (bases 1 to 39565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence AL032671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368 (6466), 32-38 (1994)
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KRVEIALRMVDFTVFIPVMDSVMDSYLDPDRDSIMFSDLFVGGTOTYCGNVTGPPAYW
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SHSNIHLWIGGDMKPBSTSANEDIFFMHHSFVDYLMELMRQLQOPRWLERQAYSADHP
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ELAKEYSVNGTKVERVPLYKRISIKMTAPLFVDCYNRAPGCCSSWAAKNGGCGREPEFMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"similar to Common central domain of tyrosinase; CDNA EST EMBL: 214371 comes from this gene; CDNA EST CEMSG81F comes from this gene; cDNA EST EMBL: M89185 comes from this gene; cDNA EST EMBL: C13572 comes from this gene; cDNA EST EMBL: C13572 comes from this gene; cDNA EST yk240all.3 comes from this gene; cDNA EST yk240all.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(3510. .3749,3844. .4023,4219. .4319,4374. .4998. .5101,5288. .5683,5730. .6167,6215. .6358)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Caenorhabditis elegans"
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/gene="K08E3.2"
complement(join(6755..6953,7015..7141,7190..7388,7618..7680,7727..7969))
/gene="K08E3.2"
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SHEDREGNGOIMLMELKSMLONGGEKMTNOEARALKPATGLDTI YRALINFNIKFTLDH
SAIGFLRTINGFEDVOMIFVSRFFTVODPSNALLKPATGLDTI YRALINFNIKFTLDH
SAIGFLRTINGFEDVOMIFVSRFFTVODPSNALLKPATGLDTI YRALINFNIKFTLDH
SAIGFLRTINGFEDVOMIFVSRFFTVODPSNALLKPATGLDFEEKLGGFSKEKAAIEE
EYSTKLRSLAKKYAKKSEEDDEILKSVSYTSSFNSFLOQLDOIATRHOTSAEHIRGGV
VSYVASKTCOMRSSRKNAINDLKTINDKLEDQINEMCKSGKCYLKSFKDAENSYOKFY
VSYVASKTCOMRSSRKNAINDLKTINDKLEDQINEMCKSGKCYLKSFKDAENSYOKFY
KADKNIEISRLELEKARALANARNEACELAKODYSALMYRTINSADKRFHYELLPVIFA
RLKAUNKECIADMRQVLOKIVSTODSLADSTEECRKIMOFEVGKIDAEGDAOLVLKSV
EATIEOPAFFELEDLGDPKNCDSRTNDSADGSGGKLLKSSPSKNRIIRNEGITRLOQAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"predicted using Genefinder; similar to EF hand, Src homology domain 3; CDNA EST EMBL:D64948 comes from this gene; CDNA EST EMBL:D6852 comes from the ST EMBL:D6852 comes from this gene; CDNA EST EMBL:D76408 comes from this gene; CDNA EST EMBL:D76408 comes from this gene; CDNA EST EMBL:D68217 comes from this gene; CDNA EST EMBL:D68217 comes from this gene; CDNA EST EMBL:D13458 comes from this gene; CDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene; cDNA EST EMBL:C13450 yk273e3.5 comes from this
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Join(14167. .14295,14596. .14763,14810. .14911,15156. .1:

15357. .15472,15552. .15645,15694. .15854,15902. .16007,

16055. .16259,16305. .16386,16433. .16509,16656. .16905,

17201. .17352,17487. .17593,17642. .17692,18137. .18266,

18350. .18524,18574. .18631)
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TTRSMSGSSTNQSSSKTIEDVLSGEAGNSSSADDSSKNILRQLFTTPKRLISSPKTSK
SSTPTPLRRRAEISSPKILRSSFSGAIRKSLSTPDSVKVETAVTVTALFEFAKSSAET
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/PVSKSPAPVSKSLALEKDEDVEKKKEKEEKEEEKGEKKEEKKDDSKEDKKD
EDHEKKKTAEEKENNEKKKEEKKDEKKKKKEEKEATEK
DDKKAKSMISVDAPELIFERTITSQKKLLLKNLTAKKVMFKIKCSSVNVYFINPVFGK
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/db_xref="PID:e1348002"
/db_xref="PID:93878441"
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yk273e3.3 comes from this gene"
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15357..15472,15522..15645,15694..15854,15902..16007,
16055..16259,16305..16386,16433..16509,16655..16905,
17201..17352,17487..17593,17642..17692,18137..18266,
18350..18524,18568..18631)
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/db_xref="PID:g3878436"
/db_xref="GI:3878436"
KADKNLEISRLELEKARALANARNEACELAKQDYSALVRKTNAEQKRYHVELLPVIFF
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/translation-"MFEKVKVSTCFHVTLLKDYIVFYVSNNLNFASRWPRRRRGORLL
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COSSILIA COMPASSING CO
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EATIEDAPFEIEDLGDPKNCDSKTNDSADGSGGKLKKSSPKKNIIRNFLGILKKKE
ADEKDEASNNDQLMYTDKSKPAHVRLSGLRSKIRDMEKQLEQATOGREGITRLQQAY
TNPQHGNPSACTEPLISYAKKIEKLKMIHNLKEFYAMLEMSVEEGQERSFGGRDPD
TTRSMSGSSTMQSSSKTIEDVLSGEAGNSSSADDSSKNILRQLFTPKRLISSPKTSK
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MSIEQGEILLVLEHDHGDGWTRTKKKHNEESGFVPTSYLQFPQ"
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/protein_id="CAB04592.1"
/db_xref="PID:e1347999"
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Query Match Local 93; Similarity Conservative 10.8%; Score 39.6; DB Pred. No. 4.2; 0; Mismatches 0 В 36; 99; Length 39565; Indels 0; Gaps 0

23 AATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTG 82 ATTCAAATTTTCTGAGAAATCATTTTGGCGGGAATTCAAATTTTAATTTTTTAAAAATAT 8564

TGTTGCAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGC 142 TTTGGCGGGAATTAAAATTTTAATTTTTTGAAAATATTTTGGCGGGAATTTAAAATTTT 8624

Sgo

203 AG 8686

Caenorhabditis elegans clone Y119ClAA, unordered pieces.
AC006710 Caenorhabditis elegans HTG; HTGS_PHASE1. Caenorhabditis elegans AC006710.1 GI:4263228 WORKING DRAFT SEQUENCE,

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REFERENCE
AUTHORS
TITLE
JOURNAL
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AC006712
JOURNAL REFERENCE
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Best Local
                                                         AUTHORS
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 Unpublished 2 (bases 1
                                     1 (bases 1 to 299919)
Waterston,R.H.
The sequence of Caehorhabditis elegans clone
                                                                                         Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda,
Rhabditina, Rhabditodea, Rhak
                                                                                                                                                                                                                                                                 AC006712 299919 bp DNA HTG 23-FEB-1999 Caenorhabditis elegans clone Y119C1b, WORKING DRAFT SEQUENCE,
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Waterston, R.H.
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                                                                                                                                                                        HTG; HTGS_PHASE1
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                                                                                                                                                                                                                                                  unordered pieces.
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/db_xref="taxon:6239"
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Rhabditidae; Peloderinae; Caenorhabditi
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Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhab
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Caenorhabditis elegans
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CEY111B2_2 200001 310000
CEY111B2_3 300001 410000
CEY111B2_3 400001 510000
CEY111B2_5 500001 610000
CEY111B2_5 500001 610000
CEY111B2_6 600001 613487
Continuation (2 of 7) of CEY111B2 from base 100001 (298857 Caenorhabditis elegans
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                            83 TGTTGCAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGC 142
                                                                                                                                            23 AATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTG 82
TTTGGCGGGAATTCAAATTTTAATTTTTTTGAAAATATTTTGGCGGGAATTCAAAATTTA 6078
                                                                                              ATTCAAATTTTCTGAGAAATCATTTTGGCGGGÄTTTCAAATTTGAATTTTTTTTTGAAATAT 6018
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On Jun 1, 1999 this sequence version replaced gi:4877274.
Order of segments is not known; 800 n's separate segments.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coll, yeast, vector,
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* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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/db_xref="taxon:6239"
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Search completed: September 25, 1999, 23:25:10 Job time: 6653 sec

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GCTCTTTCTCTCCCCCTCCTC.....CTGTGACTTGAAGTTTAGTC 366

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GenCore version Copyright (c) 1993 - 1998

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September 25, 1999, 09:55:55; Search time 273 Seconds (without alignments) 335.422 Million cell updates/sec

Scoring table:

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Database :

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score Pred. No.

No. is the number of results predicted by chance to a greater than or equal to the score of the result bear s derived by analysis of the total score distribution

to have a being printed,

SUMMARIES

Searched:

311585 seqs, 125096042 residues

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366 366 335 335 10322

V58588 V61203 V58614 V61229 V74409 Q21188 Q03253 N90843 V72993

Prostate tumour sp cDNA sequence of p Staphylococcus aur

Prostate tumour Description

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Staphylococcus aur Continuation (8 of Anther-specific ES

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V58614 standard; cDNA; 335 I
V58614;
08-DEC-1998 (first entry)
Prostate tumour specific ger
Prostate tumour specific ger
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WO937033-A2.

27-AUG-1998.
25-FEB-1998; U3-020956.
09-FEB-1997; US-806099.
01-AUG-1997; US-904804.
(CORI-) CORP.
Dillon DC, Xu J;
WPI; 98-60986/51.
therapy; ss.
Homo sapiens.
WO9837418-A2.
27-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 85; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itse can be used as a vaccine for the treatment of prostate cancer. The I was identified by analysis of a subtracted cDNA library with a normal tissue cDNA library.
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Matches 265
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09-FEB-1998; US-904
25-FEB-1997; US-806
01-AUG-1997; US-904
(CORI) CORIA CORP
Dillon DC, Xu J;
WPI; 98-480805/41.
                                                                                                                                                                                                                                                                      25-FEB-1998; U03492.
09-FEB-1998; US-0209:
25-FEB-1997; US-8060:
01-AUG-1997; US-90488
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9837093-A2.
27-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for detecting and treating prostate cancers

Claim 1; Page 100; 141pp; English.

This sequence represents a human prostate tumour specific gene, and car

be used in the method of the invention. The method is for detecting

prostate cancer comprises contacting a biological sample with an agent

able to bind an immunogenic portion of a prostate protein (such as

encoded by this sequence). An antibody which binds to an immunogenic

portion of the prostate protein, and the method can be used to detect,

monitor progression of, or treat prostate cancers. The antibody may

also be conjugated to a therapeutic agent for use in therapy of prostate
                                 Polypeptides comprising immunogenic portions of prostate protein used in a vaccine for the treatment of prostate cancer Claim 3; Page 94; 130pp; English.
The present sequence is a new DNA which encodes an immunogenic prostate tumour protein. The encoded immunogen, or the DNA can be used as a vaccine for the treatment of prostate cancer. I was identified by analysis of a subtracted CDNA library obtained was identified by analysis of a subtracted CDNA library obtained by analysis of a subtracted con the treatment of the content of the content
subtracting a prostate tumour cDNA expression tissue cDNA library.
                                                                                                                                                                                                         Dillon DC, Xu J;
WPI; 98-609886/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequence of prostate tumour clone.
Prostate; cancer; tumour; vaccine; immunogen; clone;
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Best Local Similarity
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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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Computer readable the invention. The DNA sequences are recorded on a computer readable of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are clikely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The composition against S.aureus infection of S.aureus in asample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.

Sequence 10322 BP; 3655 A; 1302 C; 1989 G; 3014 T;
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-786519-A2.
30-JUL-1997;
07-JAN-1997; 100117.
05-JAN-1995; US-009861.
(HUMA-) HUMAN GENOME SCI INC
                                                                  exon
                                                                                                                                                                                                 Sequence encoding a 302 amino region, from plasmid pCH3.5. Pest-resistant plant; transfor
                                                                                                                                                                                                                                                                       Q21188
Q21188;
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                                   intron
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                                                                                                                                                                     Tomato
                                                                                                                                                                                        nematode;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTCCTCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGA 73
                                                                                                                                                                                                                                                                                         standard; DNA; 3012
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                            /*tag= a
2384 . .2443
/*tag= b
2444 . .2597
/*tag= C
2598 . .2677
                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                      plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10322;
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Gaps

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9275

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Q0325/C
ID 203/C
ID 203/C
Q032
AC Q03
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Best Local S
Matches 91
                           making.
control
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Sequence 3012 BP; 965 A; 634 C; 436 G; 977 T;
  Sequence
                                                                                                         Disclosure; Fig 8; 41pp; English. Beta-1,3-glucanase is involved in
                                                                                                                                                                                      Recombinant DNA encoding beta-1,3-glucanase useful in plant protection and biomass conve
                                                                                                                                                                                                                                        31-JAN-1990.
20-JUL-1988; BI0555.
29-JUL-1988; US-353312.
(CIBA) CLba Geigy AG.
Shinshi H, Wenzler H, Hofsteenge J, Ryals
WPI; 90-031717/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-1990 (first entry)
Sequence of clone pBSGluc39.1 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q03253 standard; DNA; 4483
Q03253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant protein with endo chitinase activity encoding it and plants which express it, resistant to insects, bacteria and nematodes.

Example: Fig 2: 82pp; French.

The inventors claim a new recombinant gene which codes.
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(ERAP ) SOC NAT ELF AQUITAINE.
Dubois M, Grison R, Leguay JJ, Pignard A, Toppan WPI; 92-064950/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-1,3-glucanase; papermaking;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; R20820
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24-JUL-1991;
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                                                                                                                                                                from tobacco.
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                                                 La-1,3-glucanase is involved in plant defence against pathogens and
hydrolyses polyssaccharides, useful in biomass conversion or paper
king. The clones allow for transfer of the gene to other species and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGATGTATATTGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGT 129
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91; Conservative
     gene
        BP;
                              expression.
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                                                                                                                                                                                    conversion pref. is
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  744 G;
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Best Local S
Matches 75
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                                                                                                                                                                                                                                                                                     Matches
                   25-FEB-1999 (first entry) Tobacco basic beta-1,3-glucanase genomic DNA clone pBS-Gluc39.1. Regulation; transcription; plant tissue; chimeric construction; pathogenesis-related protein; anti-pathogenic; transgenic plant; beta-1,3-glucanase activity; pest resistance; ss.
                                                                                                                                                 4361
                                                                                                                                                                                                                                         4481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-1989; 103888.
08-MAR-1988; US-165667.
(CIBA) Ciba Geigy AG.
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                                                                                                                                                                                                                                                                                                                                            See also N90368, N
Sequence 4483 BP;
                                                                                                                                                                                                                                                                                                                                                                           Claim 79; page 72-74; 117pp; English. Sequence is a chemically inducible gene used transcription of an associated DNA sequence is
                                                                                                                                                                                                                                                                                                                                                                                                             and processes for inducible expression resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tobacco basic beta-1,3 glucanase Tobacco basic beta-1,3 glucanase; Nicotiana tabaccum cv. Xanthi.
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N90843 standard;
Nicotiana sp. US5847258-A.
                                                                                      V72993 standard;
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Chemical induction of cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Payne G;
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                                                                                                                                                                                                                                                                                                                                                                  tissue.
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                                                                                                                                                                                            CAATTCACACGGAGCTAGTTTGTGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT
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75; Conserv
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                                                                                      cDNA; 4483
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                                                                                                                                                                                                                                                                                                                                            N90841-N90846, and P91384-P91386
P; 1418 A; 837 C; 745 G;
                                                                                                                                                                                                                                                                                              9.2%;
52.1%;
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Pred. No. 3
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; pBSGluc39.3; herbicide resistance.
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to herbicide
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   RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T DNA encoding pathogenesis-related glucanase proteins - useful for producing transgenic plants with enhanced disease or pest resistance S Example 33; Column 163-168; 169pp; English.

C The present invention describes a DNA molecule encoding a control of the present invention describes a DNA molecule encoding a pathogenesis-related (PR) protein having beta-1,3-glucanase activity celected from PR-2, PR-2, PR-N, PR-O and PR-O'. Also described are: (1) a chimeric gene comprising the above DNA molecule linked to a cherologous promoter; (ii) a vector containing the chimeric gene; (iv) a transgenic plant containing the chimeric gene; (iv) a transgenic plant. C containing the chimeric gene; and (v) a seed from the transgenic plant. The DNA molecule is used to produce transgenic plants with enhanced disease or pest resistance. The present sequence represents a tobacco basic beta-1,3-glucanase genomic DNA sequence.

So Sequence 4483 BP; 1418 A; 838 C; 744 G; 1483 T;
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Best Local 9
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31-MAY-1995; US-457364.
31-MAY-1995; US-457364.
08-MAR-1998; US-165667.
06-FEB-1999; US-329018.
24-MAR-1989; US-326672.
20-CUT-1999; US-368672.
20-CUT-1999; US-425944.
07-SEP-1990; US-632441.
21-DEC-1990; US-632441.
21-DEC-1990; US-678378.
27-SEP-1991; US-678378.
27-SEP-1991; US-678378.
27-SEP-1991; US-978197.
06-MAR-1992; US-973197.
06-APR-1993; US-042847.
12-APR-1993; US-042847.
12-APR-1993; US-042847.
13-JAN-1994; US-181271.
(NOVS ) NOVARTIS FINANCE CORP.
MOYET MB, Payne GB, Ryals JA, Wa
                                                                 US5851766-A.
22 DEC-1998.
31-MAY-1995; 456262.
31-MAY-1995; US-456262.
(NOVS ) NOVARTIS FINANCE CORP.
Harms C, Ryals JA;
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WPI; 99-080396/07.

Isolating Chemically regulatable DNA sequences in for chemically controlling expression in transform Example 33; Column 169-174; 175pp; English.
                                                                                                                                                                                 Tobacco beta-1,3-glucanase gene clone pRSGluc39.1.
Chemically regulatable DNA promoter; expression control; pesticide;
herbicide tolerance; beta-1,3-glucanase gene; ss.
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                                                                                                                                                                     Nicotiana acuminata.
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cc a plant tissue. The method allows isolation of sequences which will be cuseful for the controlled expression of genes, under the control of a chemical regulatable sequence. This is useful in plants with a cc herbicide or pesticide detoxification mechanism under the control of a cc herbicide or pesticide to give optimal tolerance. The promoter fragment is useful in plants with a cc herbicide or pesticide to give optimal tolerance. The promoter fragment is useful for controlling sequences which encode traits such as the height, shape, development, male or female sterility, and the ability cof the plant to withstand cold, heat, salt and drought. The chemical cc induction of the promoter allows the regulation of production of compounds, e.g. flavours, fragrances, playments, natural sweeteners, industrial feedstocks, antimicrobials and pharmaceuticals, by compounds, e.g. flavours, fragrances, playments, natural sweeteners, cc industrial industrial sweeteners, cc industrial flavours, fragrances, playments, natural sweeteners, cc industrial sweeteners, by compounds, compounds, e.g. flavours, fragrances, playments, natural sweeteners, cc industrial sweeteners, cc industrial sweeteners, by compounds, cc industrial sweeteners, cc industrial sweeteners, cc industrial sweeten
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EP-786519-A2.
30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus contig SEQ ID #6. Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4421
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16-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                        2401.
                                                                                                                                                                                                                                                                                                                                                                   /note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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                                                                                                                                             "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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Pred.
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RESULT 12

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Sequence 3601 BP; 1170 A; 496 C; 738 G; 1057 T;
                                                                                                                       Query Match
Best Local Similarity
Matches 67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 82; Conserv
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Fragment Name
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Barash SC, Cho
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                                                                                       205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 CCATCTTGCTTTTTTCCCCCATTGGAACTAGTCATTAACCCATCT 176
                  265 GCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
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                                                                                   CTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATTTCACCCAGACA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATAAATACATTTCTACATTCGTAAGAATCATTAAGGTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTATATTGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAAT 133
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                                                                                                                         Conservative
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On PJ, Fannon MR, Kunsch CA,
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Pred. No. 3
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                                                                                                                                        32.2; 1
No. 19;
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                                                                                                                         58;
                                                                                                                                                        <u>ب</u>
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                                                                                                                                                        Length 110000;
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X20248_09/c
Continuation (10 of 10)
WP Sequence split into:
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CDS
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X20248_03
X20248_03
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X20248_06
X20248_05
X20248_06
X20248_06
X20248_08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCA 329
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67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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/label = B2 gene
3266. .3364
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23546.
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7961.
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103118 AAGTATTTCTACAATGTTTCAAAATATTATTCAAGATTTCAAATGCCGGAACATCGCTAA 103059
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base 900001 (Borrelia burgdorferi polynucleoti
OCUS X20248 Accession X20248
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3118 AAGTATTTCTACAATGTTTCAAAATATTATTCAAGATTTCAAATGCCGGAACATCGCTAA 3059
                                                                                                             205 CTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAAACCATTTCACCCAGACA
                                      GCCTGTTTCTATCCTGTTTAATAATTAGTTTGGGTTCTCTACATGCATAACAAACCCTG 324
                                                                                CAACTCTATTCTCATAAAACAATTTTTTTGCATTCTTATCATTTCCATGATACACTGTCA
                                                                                                                                                                     Mismatches
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12-JUN-1998 (first entry)
MAGE-B cluster DNA sequence.
MAGE-B cluster DNA; testicular seminoma; cancer; screening; leukaemia;
                                     "poly-A signal for .25194
"exon 1 of B3 gene"
                                                                                                            sequence for B2 gene"
                                                                                                                                                                    gene"
                                                                                                                                                                                                                                                                                     gene"
                                                       B2 gene
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PR 25-ARR-1997; US-965111.

PR 25-ARR-1996; US-658578.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (LUDW-) LUDWIG INST CANCER RES.

PI (LUDW-) LUDWIG INST CANCER CANCER CANCER SEQUENCE. The invention provides a novel CC CALL REST CANCER CANCER CANCER CANCER SEQUENCE.

PI (LUDW-) LUDWIG INST CANCER CAN
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05-JUN-1997; U09774.
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25152.
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38148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     "poly-A signal for Bl gene"
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.33957
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39191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    improving the quality of dough
Claim 5; Page 21-2; 41pp; Japanese.
The present sequence represents a protein phosphatase gene sequence
of Saccharomyces cerevisiae. The specification describes new
S. cerevisiae in which the growth and/or the fermentation activity
is controlled at least in the range of 0-20 degrees Celsius. These
yeast are prepared by deleting the function of at least one protein
phosphatase gene. The yeast is useful in the production of dough.
Sequence 1407 BP; 434 A; 222 C; 325 G; 426 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein phosphatase gene coding supported prosphatase gene; growth; dough production; yeast; ds.
                                                                                                                     1011
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07-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New yeast of controlled activation at low temperatures - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J11042090-A.
1071 CGACATGGAAATTGATGATCTTGATACCGAATTGGA 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KANF ) KANEKA CORP.
(SHOS ) SHOWA SANGYO CO.
WPI; 99-197822/17.
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29-JUL-1997; JP-203652.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCCCC
                                                          AGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGA 236
                                                                                                                  AGTGTTCGCAATAACCACCAAAAAATTACAAGACCGCTTGAATCGTAGTAAAGATAATGA
                                                                                                                                                                             GCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA
                                                                                                                                                                                                                                    TTTTGTCCAAAGAAGGAAAAGTATTTTTGATTTCCATGATTTTTCGGATGATGATAACGA 1010
                                                                                                                                                                                                                                                                                            TGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTT 140
                                                                                                                                                                                                                                                                                                                                                          TGAATCTGAGTCACAATGGTTTGAGCGTATGAGATCAAAAAATTACAATATCCAAACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                  TGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATAT
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0; Mismatches
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Pred. No. 17;
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/FDTUS9_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
US-07-638-431-1
PCT US92-00018-1
US-07-912-900-24
US-07-855-412B-4
US-07-867-106-2
US-08-285-309-2
US-08-313-075A-29
US-08-606-789-3
US-08-502-046-24
US-08-308-887A-4
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US-08-475-427-5
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US-08-455-246-5
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US-08-456-262-5
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Compugen Ltd
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Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEO ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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CITY: Alexandria
STATE: VA
STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIA Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
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                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L
                                                  1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                  62 ATTTCACTGTGATGTATATTGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTACT 121
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                                               CTCTTTCTCTCCCCCTCCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACAC 61
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1800 Diagonal Road,
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US-08-327-94A-3

US-08-425-061-1

US-08-425-061-2

US-08-425-061-3

US-08-425-061-4

US-08-425-061-5

PCT-US95-10203-21
                                                                                                           Score 36.6; DB 2;
Pred. No. 0.19;
190; Mismatches 154;
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176461 seqs, 45838279 residues

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RESULT 2 US-08-475-427-5

tent No.

3 5, 45, 93,

INFORMATION:

TITLE OF INVENTION:

STREET:

ADDRESSEE:

COUNTRY:

20007-5109

FILING DATE:

OPERATING SYSTEM:

OLECULE TYPE:

NAME/KEY:

TOPOLOGY:

linear

STRANDEDNESS:

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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/01
FILING DATE: 21-JUL-1991
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 24-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1403 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCAAATTCTTCTATCTCTTTAACT 1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEGUAY, Jean-
APPLICANT: PIGNARD, Annia
APPLICANT: TOPPAN, Alain
                                                                                                                                                                                     TELEFAX: (202)672-5390
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 CTGGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 TGGTTTGTGAATCCATCTTGCTTTTTCCCCCATTGGAACTAGTCATTAACCCCATCTCTGAA 181
                                                                                                                                                                                                                                   NAME: BENT, Stephen A. REGISTRATION NUMBER: 29. REFERENCE/DOCKET NUMBER:
                                                                                                LENGTH: 3012 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIGNARD, Annie
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LEGUAY, Jean-Jacques
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER: US/08/475,427
07-JUN-1995
                                                                                                                                                                                                                                                                                                       24-JUL-1990
                                                        DNA (genomic)
                                                                                      single
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Best Local Similarity
Watches 91; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08181271A Patent No. 5614395
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LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                    APPLICANT
APPLICANT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UPZIP: 10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 GAATCCATCTTGCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGA 189
                                                                CITY: Hawthorne STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 CTCCCCTCCTCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACT 69
                                                                                    ADDRESSEE: ClbA CLARA PROPERTY 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
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                                                                                                                                                                                                                                             Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                     WALLU, MALLU WILLIAMS, Shericca C.
WILLIAMS, Shericca C.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TONA SECUENCES AND USES THEREOF
                                                  USA
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Ward, Eric R.
                                                                                                                                                                                                                                                                                                                 Moyer, Mary B
                                                                                                                                                                                                                                                                                                                               Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                               Duesing, John H.
Friedrich, Leslie I
Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Beck, James J
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alexander, Danny C.
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join(2167..2383, 2463..2616, 2698..3007
2698)
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1942..2166
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                                                                                                                 CIBA-GEIGY Corporation
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Pred. No. 0.74;
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                                                                                                           Query Match
                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                   NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 07/425,504
APPLICATION NUMBER:
FILING PARTS
4481
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FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA: 07/560 /21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/848,506 FILING DATE: 6-MAR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: 6-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/093,301
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APPLICATION NUMBER:
FILING DATE: 24-MAR-
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FILING DATE: 7-SEP-1
PRIOR APPLICATION DATA:
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                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
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                                                                                       y Match 9.28;
Local Similarity 52.18;
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OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                        STRANDEDNESS:
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                 1 GCTCTTTCTCCCCCCCCCCCCCCGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
 GCTCTTTTGCTGCTCTGAATAGAGTCTTCTTTCCTGCCTTTGGAGTTGATGAAATGGA 4422
                                                                                                                                                                                                                                          nucleic acid
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US 07/368,672
20-JUN-1989
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7-SEP-1990
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24-MAR-1989
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                                                                                         Score 33.6; DB 1; Length 4483; Pred. No. 1.1;
                                                                          Mismatches
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US-08-449-315-5/c
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                                                                                                                                                                                                                     CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
                         APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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APPLICANT:
APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION UMBER: US/08/449,315
FILING DATE: 24-MAY-1995
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
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                                                                                                                                                                                                        APPLICATION NUMBER:
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5. 5650505
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Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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Stinson, Jeffrey R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuhaus, Jean-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIBA-GEIGY Corporation
                                                                                                                                                                                        JMBER: US 07/678,378
1-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s, Shericca C.
CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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US 07/632,441
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AND ANTI-PATHOGENIC THEREOF

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Best Local Similarity
                                                                                                                                                                                                                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  quence 5, Applic
tent No. 5654414
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Elmer James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-9825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
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APPLICATION NUMBER: US 0:
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                    121 TTGGTTTGTGAATCCATCTTGCTT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/368,672 FILING DATE: 20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CAATTCACACGGAGCTAGTTTGTGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT 4361
                                                                                                                                                                                                                                                                    Application US/08444803
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                                                                                                              Friedrich, Leslie B
Goodman, Robert M.
                                                                                                                                                   Duesing, John H.
                                                                                                                                                                       Beck, James J
                                     Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                         Alexander, Danny C
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   George B
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Pred. No. 1.
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EILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
APPLICATION NUMBER: US 07/425,504
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FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/678,378
FILING DATE: 1-APR-1991
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APPLICANT: Williams,
TITLE OF INVENTION: (
                                                                                                                                                               FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                                       ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
                                                                                                                                FILING DATE: 24-MAR-PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/pl/CGC 1727
PLECOMMUNICATION INFORMATION:
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STATE: New York
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ADDRESSEE: 7 Skyline Drive
                                                                                            APPLICATION NUMBER: US OF FILING DATE: 12-APR-1993
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VENTION: CHEMICALLY REGULATABLE
VENTION: DNA SEQUENCES AND USES
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Stinson, Jeffrey R.
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                         NUMBER: US 07/329,018
24-MAR-1989
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20-OCT 1989
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Best Local Similarity 52.1%;
Matches 75; Conservative
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TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 5
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
                                                                                                                                                                                                                                                                                                             APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4483 base pairs
                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                       CITY: Hawthorne
STATE: New York
                                            APPLICATION NUMBER: US/08/449,043 FILING DATE: 24-MAY-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                        ADDRESSEE: CIBA CALLA PROPERTY 7 Skyline Drive
                                                                                                                                                                                                       COUNTRY:
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CATION NUMBER: 08/181,271 G DATE: 13-JAN-94
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Stinson, Jeffrey R.
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Meins, Jr., Frederick
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                                                                                                                                                                                                                                                                                                                                                                                   Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alice
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Pred. No. 1.1;
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Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 7-SEP-19
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FRIOR APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
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FILING DATE: 16-JUL-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
                                                                                                                                         SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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                                                                    4421 CAATTCACACGGAGCTAGTTTGTGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT 4362
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NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
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APPLICATION NUMBER:
                                 121 TTGGTTTGTGAATCCATCTTGCTT 144
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                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                          1 GCTCTTTCTCTCCCCCTCCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
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CCCGTTTGTTGTGGCATGCTTCTT 4338
                                                                                                                                                                                                                                                                                                                                                                                              4483 base pairs
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                                                                                                                                                                                                                Conservative
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linear
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20-JUN-1989
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US-08-456-265A-5/c
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APPLICATION NUMBER: US 08/181,271
EILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
EILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/
FILING DATE: 31-MAY-95
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                         FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
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FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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                                                                                                                                                                  APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
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FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goodman, Robert MAPPLICANT: Stinson, Jeffrey
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APPLICANT: Ryals, John A.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Tarrytown
STATE: New York
                                                                                                                               APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
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                                                         JMBER: US 07/368,672
20-JUN-1989
WBER: US 07/329,018
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Best Local (
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Williams,
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICANT:
APPLICANT:
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APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                COUNTRY:
ZIP: 105
                                                                                                            CITY: Hawthorne
STATE: New York
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Local Similarity 52.1%;
                                                                                                                           ADDRESSEE: Claaron Drive
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                                                                             10532
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Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
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Stinson, Jeffrey R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        John H.
                                                                                                                                                                                                                                                                                                                               Jean-Marc
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CURRENT APPLICATION DATA:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
CTILING DATE: 6-NOV-1992
   4481
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PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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FILING DATE: 1-APR-1991
PRIOR APPLICATION UNBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 4483 base pair
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FILING DATE: 27-SEP-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
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APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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                                                                                                                                                                                                                                                                                                                                                               NAME: Elmer, James Scott REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 12-API
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                          1 GCTCTTTCTCCCCCTCCTCTGAATTTAATTCTTTCAACTTGCAATTTTGCAAGGATTACA 60
GCTCTTTTGCTGCTCTCTGAATAGAGTCTTCTTTCCTGCCTTTGGAGTTGATGAAATGGA 4422
                                                                                          Similarity
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21-DEC-1990
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24-MAR-1989
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27-SEP-1991
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ER: S-
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                                                                       Score 33.6; DI
Pred. No. 1.1;
O; Mismatches
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                                                                                                       DB 3;
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                                                                                                       Length 4483;
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US-08-455-244-5/c
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                                                                                                                         FILING DATE: 1-APR-1991
PRIOR APPLICATION NAMEER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                             APPLICATION NUMBER:
FILING DATE: 8-MAR-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                            APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
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                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/455,244 FILING DATE: 31-MAY-1995
                                                APPLICATION NUMBER: FILING DATE: 6-APR
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08 FILING DATE: 13-JAN-94
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hawthorne
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Payne, George B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harms, Christian
Meins, Jr., Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Friedrich, Leslie B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alexander, Danny C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duesing, John H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIBA-GEIGY Corporation
                                                                                              MBER: US 07/165,667
8-MAR-1988
                                                                                                                                                                                                JMBER: US 07/678,378
1-APR-1991
                                                                                                                                                                                                                                                                                              16-JUL-1993
MBER: US 07/632,441
21-DEC-1990
                                                 MBER: US 08/042,847
6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IS, Shericca C.

CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

DNA SEQUENCES AND USES THEREOF

1 106
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                                                                                                                                                                                                                                                                                                            US 08/093,301
                                                                                                                                                                                                                                                                                                                                              08/181,271
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

US 07/425,504

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US-08-454-876-5/c
                                                                                                                                                                                                                                                     Sequence 5, Application US/08454876 Patent No. 5804693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 9.2%;
Best Local Similarity 52.1%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-193
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (919)541-8585
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE : 4483 base pairs
                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4421 CAATTCACACGGAGCTAGTTTGTGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT 4362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4481 GCTCTTTTGCTGCTCTCTGAATAGAGTCTTCTTTCCTGCCTTTGGAAGTTGAAATGGA 4422
                                                                                                                                                                                                    APPLICANT:
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REFERENCE/COCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-JUN-1989 PRIOR APPLICATION DATA:
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FILING DATE: 6-MAR-1:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                      121 TIGGITIGIGAATCCATCTIGCTI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTCTTTCTCCCCCCCCCCCTCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
                                               Goodman, Kouca
Harms, Christian
Meins, Jr., Frederick
Contoya, Alice
                                                                                                                     Duesing, John H. Friedrich, Leslie B. Goodman, Robert M.
                                                                                                                                                                                Beck, James J.
                                                                                                                                                                                                                     Ryals,
                                  Neuhaus,
                                                                                                                                                                                                Alexander, Danny C.
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6-MAR-1992
George B.
on, Christoph
                                                                                                                                                                                                                   John A.
                                  Jean-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-19825/P1/CGC 1727
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Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION NUMBER: 08/181,271
APPLICATION NUMBER: 08/181,271
APPLICATION NUMBER: US 08/93,301
FILING DATE: 13-CAN-94
APPLICATION NUMBER: US 08/93,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOY-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                      APPLICATION NUMBER: US 07,
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08,
FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION UDATA:
APPLICATION UDATA:
APPLICATION UDATA:
US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 27-SEP-PRIOR APPLICATION DATA:
                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/632,441
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S--
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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STREET: 7 Skyline Drive
CITY: Hawthorne
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                                                                                                                                                                                                                                                                                                                                 NUMBER: US 07/368,672
20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/768,122
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                                          S-19825/P1/CGC 1727
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Best Local Similarity 52.1%;
Matches 75; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equence 5, Applic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                        CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCTCTTTCTCTCCCCTCCTGAAITTAATTCTTTCAACTTGCAAITTGCAAGGATTACA 60
APPLICATION NUMBER: 08 FILING DATE: 13-JAN-94 APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ryals, John A.
Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Payne, George B. christoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stinson, Jeffrey R.
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                                                                       08/181,271
   US 08/093,301
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FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMPFO-FILING TO-
                                                                 4421 CAATTCACACGGAGCTAGTTTGTGGGGTAAGATCAAAATAGATCTCTTAGCTGGAAGTTAT 4362
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PRIOR APPLICATION DATA:
APPLICATION MINISTER STREET
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FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
ADDITIONATION FOR APPLICATION DATA:
                                                                                                                                      4481 GCTCTTTTGCTGCTCTGAATAGAGTCTTCTTTCCTGCCTTTGGAGTTGATGAAATGGA 4422
4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
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PRIOR APPLICATION DATA:
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                              121 TIGGTITGTGAATCCATCTTGCTT 144
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                                                                                          APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/768,122 FILING DATE: 27-SEP-1991
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REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4483 base pairs TYPE: nucleic acid
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                                                                                                                                                                         1 GCTCTTTCTCTCCCCCTCCTGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACA 60
                                                                                                                                                                                                                        Similarity
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20-OCT 1989
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Pred. No. 1
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US-08-456-262-5/c
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Patent No.
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APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION UMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION UMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                               FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                   APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08
FILING DATE: 31-MAY-1995
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Hawthorne
New York
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Stinson, Jeffrey R.
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US 07/768,122
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-456-262-5
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TELEPHONE: (919)541-8614
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               APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DAA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 7-SEP-1
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NUMBER OF SEQUENCES: 1
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Local Similarity 52.1%;
les 75; Conservative
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Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
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                                                                            Uknes, Scott
Ward, Eric R.
                                                                                                                                                                     Neuhaus, Jean-Marc
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Meins, Jr., Frederick
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Pred. No. 1.1;
0; Mismatches 69;
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
                                                                        TELEFAX: (919)5
NFORMATION FOR SEQ
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION NUMBER: US 07/768,122
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FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
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APPLICATION NUMBER: US
                                                   SEQUENCE CHARACTERISTICS
                                                                                                                         REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NUMBER: US 07/165,667
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 6-MAR-1992
STRANDEDNESS:
                                                                                                            TELEPHONE:
                                                                                                                                                             NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                       APPLICATION NUMBER:
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T: 7 Skyline Drive
Hawthorne
: New York
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                                                                                         : (919)541-8614
(919)541-8689
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N NUMBER: US 07/425,504
E: 20-OCT 1989
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24-MAR-1989
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20-JUN-1989
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21-DEC-1990
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Best Local Similarity 52.1%;
Matches 75; Conservative
                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,736
FILLING DATE: 31-MAY-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271
FILLING DATE: 13-JAN-1994
APPLICATION NUMBER: US 08/093,301
FILLING DATE: 16-JUL-1993
PRIOR APPLICATION NUMBER: US 08/093,301
FILLING DATE: 16-JUL-1993
PRIOR APPLICATION NUMBER: US 08/093,7197
FILLING DATE: 6-NOV-1002
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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FILING DATE: 6-NOV-1992
PRIOR APPLICATION UMBER: US 07/678,378
FILING DATE: 1-APR-1991
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APPLICANT
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APPLICANT
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: New York
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Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                        USA
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Stinson, Jeffrey R.
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Friedrich, Lesl
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Payne, George B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                Floppy disk
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Pred. No. 1.1;
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                                                                                                                                                                                                                             RESULT
                                                                                                         Sequence 1, Application US/08455073A Patent No. 5876949
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Best Local Similarity 52.1%;
Matches 75; Conservative
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APPLICATION NUMBER: US 08/04:
EILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 35,129
REFERENCE/DOCKET NUMBER: S-19
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF THE LECT 
                                                                           GENERAL INFORMATION:
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[NFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/200 0000
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APPLICANT: Gideon Dreyfuss
APPLICANT: Mikiko C. Siomi
                                                                                                                                                                                                                                                                                                                                  4361 CCCGTTTGTTGTGGCATGCTTCTT 4338
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APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
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APPLICATION NUMBER: (
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TOPOLOGY: 11
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6-FEB-1989
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Pred. No. 1.1;
0; Mismatches 69;
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Query Match
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US-08-455-073A-1
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SOFTWARE: WORDERFIECT 6.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/455,073.
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2201
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10508-3100
TELECOMMUNICATION 10508-3100
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                       3322 AAAAAACAAAAGAAAAAAAGAAAAAAAGTTGTTATTTGTTAACCGATCTTAGTCTTTTC 3263
3262 CAATTCTGCTTAAACATTAGACCATATATTTCAAAGTTTACAAA 3219
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TITLE OF INVENTION: Fra
TITLE OF INVENTION: Of
NUMBER OF SEQUENCES: 1:
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                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
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                                150 CCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAA 193
                                                                                                      90 AAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
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ZIP: 19103
                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                              Mismatches
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Search completed: September 25, 1999, 07:29:06 Job time: 3383 sec

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Title:
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366
1 GCTCTTTCTCTCCCCT
    September 25, 1999, 12:05:02; Search time 1811.29 Seconds
(without alignments)
398.582 Million cell updates/sec
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em_est3: *
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58.	57:	56:	55:	54:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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031 qc22e1 769 tf09g0	31255 nj09a12. 77355 zi58e10	28104 nj15a05.	95410 we79g06.	23843 tg35c04.	18326 gĥ16d03.	22798 np77b06.	201254 af70h05.	79219 nf36a08.	017701 0m42T12.	52376 ns52h09.	376 wb91f07.	27743 ng95e05.	50230 ns93e02.	40241 nr20h08.	28941 nc35h08.	54919 nt77e01.	418 zu69q10.	03372 np06d01.	508806 nh69c06.	758204 ah68e11.	692186 wd37a02.	543 a136b07.	027196 0v83a09	424280 tf01g02	507804 pg89g12	7390 2030b11 01	104 nsyzIII.	93522 ng75f05.	31606 nj65e04.	772 nj93c05.	72753 we58d10.	928 nr28d08.	29495 nc35a03.	85682 ++89603	37224 zv54b10	813366 a444603	20178 tu54all.	972883 op24g07.	nescription	

ALIGNMENTS

VERSION	ACCESSION NID		DEFINITION	LOCUS .	AA972883/c	RESULT 1
AA972883.1 GI:3148063	AA972883 g3148063	IMAGE:1577820 3', mRNA sequence.	op24g07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone	AA972883 455 bp mRNA EST 07-JUL-1998		

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JOURNAL COMMENT
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AUTHORS
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SOURCE
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    362 TAGTC 366
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                                                                                                  CTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTT 361
                                                                                                                                            TGGTTTGTGAATCCATCTTGCTTTTTCCCCCATTGGAACTAGTCATTAACCCATCTCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 633 Std Error: 0.00
Seq primer: -40mil fwd. ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soares and M. Fatima Bonaldo. 68 c 94 g 131 t
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/ob_xref="taxon:9606"
/clone="IMAGE:1577820"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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Pred. No. 8.7e-74;
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                                               ATTTCACTGTGATGTATTGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTACT
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Unpublished (1997)
On Mar 10, 1998 this sequence version replaced g1:2949075
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tu54a11.x1 NCI_CGAP_Pr28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 538)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_PT22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-12206I5).
Subtraction by Bento Soares and M. Fatima Bonaldo.

84 c 113 g 151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:2254844"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Pr28"
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100.0%;
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                                                                                                                                                                                                                                                                                    Length 538;
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em_est8:*
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                em_est19:

9b_est2::

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9b_est10::

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

KEYWORDS		NID	ACCESSION	Š	LOCUS	T97/CCTW
ESST.	AI557281.1 GI:4489644	9,4489644	AI557281	PT2.1_15_G12.r tumor2 Homo sapiens cDNA 3', mRNA sequence.	AI557281 777 bp mrNA EST 23-MAR-1999	

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JOURNAL COMMENT
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Best Local Similarity
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                                                                                   GTGAGCTCACGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Washington
Department of Molecular Biotechnology,
Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 777)

Huang,G.M., Ng,W., Farkas,J., Chen,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate Cancer Expression Profiling by cDNA Sequencing Analysis Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3138767.
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Location/Qualifiers
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205 c 227 g 157 t 26 others
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/db_xref="taxon:9606"
/map="960H11; 6; 6p21.31-6p22.1;
/clone_lib="tumor2"
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81.9%;
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                                                                - CAGAATGCTACCGTGCTGCAGTGCGTGAACGTGTC
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                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodr
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G. E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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AA503963.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
On May 8, 1995 this
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 404)
                                                                                                                                                                                                                                               Insert Length: 1244 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (301) 496-1550
               64
          /clone_lib="NCI_CGAP_Pr5"
/sex="male"
                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:954696"
                                                                                                                                                                                                                                 Location/Qualifiers
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Ph.D. Rodrigo

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Sequencing (information

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g1:801235

Project (CGAP),

Mammalia;

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Best Local Similarity
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1 (bases 1 to 569)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAI Tumor Gene Index Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
AI686689
g4897983
                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Elmail: Robert_Strausberg@nih.gov
Elmail: Robert_Strausberg@nih.gov
Elmail: Brownstein, M.D., Ph.D., Michael R.
Elmmert_Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI686689 569 bp mRNA EST 27-MAY-1999 tu35g11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253092 3'similar to TR:Q92046 Q92046 PREPROTRYPSIN PRECURSOR;, mRNA
                 Seq primer: -40UP from Gibco High quality sequence stop: '
                                                                 www-bio.llnl.gov/bbrp/image/image.html
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quality sequence stop: 444.
Location/Qualifiers
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Pred. No. 2.2e-76;
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||||||||||||||
TCGGAAAAGCCCC 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCCGCTGTACCACCCCAGCATGTTTTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCCT
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           nj55e05.sl NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:996416 similar to SW:KLKA_MOUSE P15946 GLANDULAR KALLIKREIN K11 PREC
                                                             human.
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/clone_lib="NCI_CGAP_Pr28"
/sex="male"
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/lab_host="DH10B"
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Pred. No. 1.1e-66;
0; Mismatches 1;
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                                ----CAGAATGCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGTCTGAGGAGGTCTG
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   CCAGAAGGACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTGCA 628
                                                                                                                                   AGGCAGAATGCCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGGTGTCTGAGGAGGTCTG 508
                                                                                                                                                                                                                                                                      Seq p
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cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ert Length: 640 Std Error: 0.00 primer: -40ml3 fwd. ET from Amersham h quality sequence stop: 412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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Pred. No. 2.2e-64;
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 GCAGGGCCTTGTGTCTTTCGGAAAAGCCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTA
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Query Match
Best Local Similarity
626 GCAGGGCCTTGTGTCTTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTA 685
                                                                                                    GACCAGAAAGGACTCCTGCAACGGTGACT-CTGGGGGGCCCCCTGATCTGCAACGGGTACTT 625
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AA533140
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1 (bases 1 to 576)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
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On Sep 12, 1996 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                        /note="Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:995579"
/clone_lib="NCI_CGAP_Pr9"
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/lab_host="DH10B"
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                                                                                                                           115 AACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAGAGCCAGGGAGC 174
              235 AACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGC
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                                             CAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCCAGAGTACAACAGACCCTTGCTCGCT 234
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                                                                                                            AGCTTCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAGAGCCAGGGAGC 174
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1 (bases 1 to 722)

Huang,G.M., Ng,W., Farkas,J., Chen,L., Liang,H.A., Gordon,D., Jun Yu,J. and Hood,L.

Prostate Cancer Expression Profiling by cDNA Sequencing Analysis Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Washington
Department of Molecular I
Washington, Seattle, WA 1
Tel: 5106280100
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PT2.1_10_F05.r tumor2 Homo sapiens cDNA
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AI557025.1 GI:4489388
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                                                                                                                                                                                                                                                              /map="15; 21q"
/clone_lib="tumor2"
/note="Organ: Prostate; Vector: pBluescript; Directional
/note="Organ: Prostate; Vector: pBluescript; Directional
cDNA library was constructed using Lambda ZP II kit
(Stratagene). mRNA was extracted from a frozen prostate
tumor tissue (Mayo Clinics)."
156 c 195 g 176 t 49 others
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/db_xref="taxon:9606"
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Pred. No. 1.1e-48;
Pred. No. 26;
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nk52c07.sl |
similar to
                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Kriaman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 259)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                               Insert Length: 458 Std Error:
Seq primer: -40ml3 fwd. ET from
High quality sequence stop: 258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g2336800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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    56
                                    prostate intraepithelial neoplasia (high-grade), cDI made by oligo-dT priming. Non-directionally cloned Size-selected on agarose gel, average insert size (
                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="17q21"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                               /note="Organ: prostate; Vector: pamp10; mRNA made from
                                                                                                                   /tissue_type="low-grade prostatic neoplasia"
/lab_host="DH10B"
                                                                                                                                                                         /clone="IMAGE:1017132"
/clone_lib="NCI_CGAP_Pr7"
                                                                                                                                                           /sex="male"
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NCI_CGAP_Pr7 Homo
contains MSR1.b3
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106 g
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Homo sapiens cDNA clone IMAGE:1017132
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Query Match
Best Local Similarity 88.8
Matches 231; Conservative

16.5%;

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Score 209.2; DB : Pred. No. 4.2e-41; 0; Mismatches 28

DB 35;

Length

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AA552779/c
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                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
On Jan 25, 1995 th
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 229)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
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                                                                                                                                                                                                                                                                                                                                                                Insert Length: 419
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      49
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                                                            /note-"Organ: prostate; Vector: pAMP10; mRNA made from prostate intraepithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned.
                                             Size-selected
                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1017594"
/clone_lib="NCI_CGAP_Pr7"
                                                                                                                              /tissue_type="low-grade prostatic neoplasia"
/lab_host="DH10B"
                                                                                                                                                                         /sex="male"
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    38 c
    94 g
                                             on agarose gel, average insert size 600 bp
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AA603977/c
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Best Local Similarity
Matches 207; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1395285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA603977 241 bp mRNA EST 28-OCT-1997 no47a09.s1 NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1103800 3' similar to contains MSR1.b3 MSR1 repetitive element;, mRNA
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                     primer: -40ml3 fwd. ET from Amersham quality sequence stop: 231.
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/clone="IMAGE:113800"
/clone=lib="NCI_CGAP_Pr23"
/clone=lib="NCI_CGAP_Pr23"
/sex="male, pooled"
/tissue_type="prostate tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: prostate; Vector: Bluescript SK-; Site_1:
Primer:
BCORRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled prostate tumors. 5' adaptor sequence: 5
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                              organism-"Homo sapiens"
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Pred. No. 7.6e-39;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TCCCTCAGACCCAGCGGTCCAATGCCACCTAGACTCTCCCTGTAAACAGTGCCCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GAGGTCCAGGCCCCCAACCCCTCCTTCCCCAGACCCAGAGGTCCAGGTCCCAGCCCCTCC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGAAATAAAGTCTAAGAGAAGCGCAAAAAAAAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAAATAAAGTTTAAGAGANGNGCAAAAAAAAAA 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACGTTGACCCAACCTTACCAGTTGGTTTTTCATTTTTGTCCCTTTCCCCTAGATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI674521 218 bp mRNA EST 19-MAY-1999 wc39g02.x1 NCI_CGAP_Fr28 Homo sapiens cDNA clone IMAGE:2321042 similar to contains MSR1.t2 MSR1 repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On Mar 16, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 218)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                    Seg primer: -40UP from Gibco
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/note-"Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification,
                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2321042"
                                                                              /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                      /clone_lib="NCI_CGAP_Pr28"
                                                                                                                        /sex="male"
                                                                                                                                                                                                                                ocation/Qualifiers
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92.1%;
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Pred. No. 3.8e-37;
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MEDLINE
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EST40886
                     The Institute for Genomic Research 9712 Medical Center Drive, Rockvil Tel: 3018699056
                                                                            Bioinformatics
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1098 GTCCCAGCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCACCTAGATTTTCCCTGNACA 1157
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                                                                                                                          Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
Contact: Kerlavage, AR
                                                                    On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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90.8%;
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Pred. No. 5.
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.8e-37;
                                                                    replaced gi:692773
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end similar to
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Rockville,

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20850 USA

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JOURNAL COMMENT
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Best Local Sim:
Matches 176;
                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                     Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Sec primer:
                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
A1675815
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wb97b12.x1 NCI_CGAP_Pr28
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hg1/hg1.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 188)
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                                       www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                             published (1997)
Dec 20, 1995 this sequence version replaced gi:1133540
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Site_1: EcoRI; Site_2: XhoI"
a 65 c 63 g 38 t 5 others
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/db_xref="ATCC (inhost):138014"
/db_xref="taxon:9606"
/clone_lib="Endometrial tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
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IMAGE:2313599
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                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 191)
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AA595489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no34h04.sl NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1102615 3',
                                                                                                 Tissue Procurement: L. J. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                              On Apr 14, 1993 this sequence version replaced
                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xref="taxon:9606"
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92.9%;
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Pred. No. 5.6e-31
0; Mismatches 1
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1093 TNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCAACCTAGATTTTCCCT 1152
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National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
On Nov 29, 1993 this sequence version replaced of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue_Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 507)
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                                 Insert Length:
                                                                                                    www-bio.lini.gov/bbrp/image/image.html
                                                                                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NA583052.1
                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D.
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/tissue_type="prostate tumor"
/lab_host-"Solk (kanamycin resistant)"
/note="Organ: prostate; Vector: Bluescript SK-; Site_1:
/note="Organ: prostate; Vector: Bluescript SK-; Site_
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/clone_11b="NCI_CGAP_Pr23"
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/db_xref="taxon:9606"
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Pred. No. 5.1e-28;
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AA293027
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AUTHORS
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                Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-Merck EST Project 1997
Unpublished (1997)
Un Nov 29, 1993 this sequence version replaced gi:636296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA293027 517 bp mRNA EST 12-AUG-1997 zt54a12.rl Soares ovary tumor NDHOT Homo sapiens cDNA clone IMAGE:726142 5' similar to TR:G940540 G940540 SERINE PROTEASE
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                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                         4444 Forest Park Parkway,
                                                                                                                                                                                                Contact: Wilson RK
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High quality sequence stop: 457
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4)."
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/clone_lib="NCI_CGAP_Co9"
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/db_xref="taxon:9606"
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Pred. No. 2.2e-18;
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Best Local Similarity 61.2%;
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/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary: Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5' strand cDNA was primed with a Not I - oligo(dT) primer [5' stranded cDNA was size selected, ligated to Eco RI double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "

(Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
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1. .517
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/db_xref="GDB:5938189"
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/sex="Female"
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/clone="IMAGE:726142"
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87 Human DNA 31714 Human C 01549 Human C 06 Human DNA 05143 Homo sa 1584 Human DN	Hon Hon	7371 Homo sapie 01 Homo sapie 8600 Homo sapi 046 Homo sapi 1114 Homo sapi 1190 Homo sapi 303 Homo sapi 303 Homo sapi	Homo sap	AF148532 Homo sapi AF113141 Homo sapi AF113140 Homo sapi AL03158 Homo sapi AC002765 Human BAC AC007728 Homo sapi AC002429 Human BAC AC007160 Homo sapi AC006960 Homo sapi AC004824 Homo sapi

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ALIGNMENTS

FEATURES		JOURNAL	AUTHORS	REFERENCE	JOURNAL		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	NID	ACCESSION	DEFINITION	LOCUS	AF135023	RESULT 1
Location/Oualifiers	Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5, Canada	Submitted (13-MAR-1999) Pathology and Laboratory Medicine, Mount	Yousel, G.M., Luo, L.Y. and Diamandis, E.P.	2 (bases 1 to 4740)	Biochem. Biophys. Res. Commun. (1999) In press	19q13.3-q13.4	Identification of novel human kallikrein-like genes on chromosome	Yousef, G.M., Luo, L.Y. and Diamandis, E.P.	1 (bases 1 to 4740)	Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	Homo sapiens	human.		AF135023.1 GI:4589272	94589272	AF135023	Homo sapiens kallikrein-like protein 1 KLK-L1 gene, partial cds.	AF135023 4740 bp DNA PRI 20-APR-1999		

Result No.

Query Score Match Length DB ID

Description

AF135023 Homo sapi

1411.4

96.7

4740 42 AF135023

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 1s derived by analysis of the total score distribution.

SUMMARIES

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ACACAGGGCCGCATGGCGAGATGCAGAGATGGAGAGACACACAGGGAGACAGTGACAACT
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                     ACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCCTGCAACGTGA
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/product="kallikrein-like protein 1 KLK-L1"
/protein_id="AAD26424.1"
/protein_id="AAD26424.1"
/db_xref="PID:94589273"
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/db_xref="GI:4589273"
/translation="SLYSGSCSQIINGEDCSPHSQPMQAALVMENELFCSGVLVHPQWVLSAAHGFQNSYTIGLGLHSLEADQEPGSQMVEASLSVRHPEYNRPLLANDLMLIKLD ESVSESDTIRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLOCVNVSVVSEEVCSKL YDPLYHPSMFCAGGGQDOKDSCNGDSGGPLICNGYLQGLVSFGKAPCGQVGVPGVYTN LCKFTENIEKTVQAS"
1275 c 1308 g 1051 t
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join(<2263. .2425,2847. .3097,3181. .3317,4588.
/product="kallikrein-like protein 1 KLK-L1"
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/organism="Homo sapie
/db_xref="taxon:9606"
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2 (bases 1 to 4385)
Stephenson, S.A., Ashworth, L. and Clements, J.A.
Direct Submission
Submitted (03-MAY-1999) School of Life Science,
University of Technology, George Street, Brisban
                                                                                                    1 (bases 1 to 4385)
Stephenson, S.A., Verity, K., Ashworth, L. and Clements, J.A.
Localization of a new prostate specific antigen-related serine
protease gene, KIK4, is evidence for an expanded human kallikrein
(KLK) gene family cluster on chromosome 19q13.3-13.4
Unpublished
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4385)
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/CRAINWENELFCSGVLIVHPOWVLSAARCFQNSYTIGLGLHSLEADQEPGSQMYEASLS
VRHPEINRFLLANDLMLIKLDESVSESDIIRSISIASQCFTACRSCLVSGWGLLANGR
MPTVLQCVNVSVVSEEVCSKLYDPLYRPSMFCAGGGQDQXDSCNGDSGGPLICNGYLQ
GLVSFGKAPCGQVGVPGVYTNLCKFTEWIEKTVQAS"

1184 c 1192 g 996 t
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/product="kallikrein
<551. .>4352
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4200. .>43
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join(551. .611,1875. .
/gene="KLK4"
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/protein_id="AAD38019.1"
/db_xref="PID:g5020096"
/db_xref="GI:5020096"
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/db_xref="taxon:9606"
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                                                                                                                  145 CCTTGCTCGCTAACGACCTCATGCTCATGCAGGTTGGACGAATCCGTGTCCGAGTCTGACA 204
                                                                                                                                                                                                                               212 ACTGTTTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAG 271
     272 AGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCCAGAGTACAACAGAC
                                                                                                                                                                              85 AGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCCCCGTACGGCACCCCAGAGTACAACAGAC 144
                                                                                                                                                                                                                                            25 AGTGAGTGCAGAGCTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAG
                                                   CCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCCTCGTTT 264
                                                                                                 CCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACA 391
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Submitted (10-DEC-1998) Chiroscience
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1 (bases 1 to 1347)
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VRHPEYNRPLLANDLMLIKLDESVSESDTIRSISIASQCPTAGNSCLYSGWGLLANGR
MPTVLQCVNVSVYSEEVCSKLYDPLYHPSMFCAGGGHDQKDSCNGDSGGPLICNGYLQ
GLYSFGKAPCGQVGVPGYYTNLCKFTEWIEKTYQAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="serine protease prostase"
/protein_id="AAD21580.1"
/db_xref="PID:g4512030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:4512030"
/translation="MATAGNPWGWFLGYLILGVAGSLYSGSCSQIINGEDCSPHSQPW
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1173 TGGCTCATGCCTGTAATCCCCAGCACTTTGGGAGG-CGAGGCAGGCAGGCAGATCACTTGAGGTA 1231
                                                                                              1113 AGAGGTGAAACACGAAGAGAAAACAGGAAAAAATCAAGACTCTACAAAGAGGCTGGGCAGGG 1172
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                                                                                                                                                                                                                                                                                                                                                                                                            AL Submitted (10-JUN-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquerysanger.ac.uk Clone requests: clonerequeststanger.ac.uk
On May 27, 1999 this sequence version replaced gi:4741461.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coll, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Unfinished: dJ310013 Contig_ID: 00252 acc=AL031658
Length: 1113 bp Unfinished: dJ310013 Contig_ID: 00912
acc=AL031658 Length: 162976 bp Unfinished: dJ310013 Contig_ID:
02100 acc=AL031658 Length: 1034 bp.
* NOTE: This is a vorking draft' sequence.
* This record will be updated with the finished sequence
* the as soon as it is available and the accession number will
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1 (bases 1 to 166723)
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/db_xref="taxon:9606"
/chromosome="20"
/clone="310013"
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Human BAC clone RG030H15
AC002066
                       Direct Submission
Submitted (09-MAY-1997)
Genome Sequencing Center
Department of Genetics, Washington
St. Louis, MO 63108, USA
                                                                                        Dante, M. Wamsley, P. and Keppler, D.
The sequence of H. sapiens BAC clone RG030H15
Unpublished (1997)
2 (bases 1 to 151770)
Waterston, R.
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 151770)
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//genome.wustl.edu/gsc
l: sapiens@watson.wustl.edu
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5 from
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to egreen@nhgri.nih.gov

This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9785K. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996). VECTOR: pBELO

NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of H_RG030H15;
actual end is at 151770 of H_RG030H15. The orientation of this clone is unknown.

FEATURES misc_feature source repeat_region This clone contains complement(9403. /rpt_family="L1" complement(9481. /rpt_family="L1" /rpt_family="L1"
complement(2759.
/rpt_family="L1" complement(5317. .5615)
/rpt_family="ALU"
complement(6063. .6314)
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2. .27794 _family="ALU" family-"L1" family-"L1" .10770 Lb="CITB-978SK-B" .8152) .4468) .9434) . 8233) human EST .2781) .20712) .19055) .17675) .21785) .17485) .21001) D45516 (NID: 9662470)"

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36141. 36342
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//note="similar to human EST C18935 (NID:g1580537)"

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                                                                      GGGAGGCTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGA 1394
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                                                       GCGAATCACCTGAGGTCAAGAGTTCGAGAGCAGCCTGGCCAACATGGTGAAACCCCACCT
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                        GCCTGTAATCCCAGCACTTTGGGAGGC-GAGGCAGGCAGATCACTTGAGGTAAGGAGTTC 1239
                                                                           AGCAGCACCAAACACCATCAACAGAAAAGGACACAAAAATAGGCCGGGCACATTGGCTCAT 111609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * by the finished sequence as soon as it is available and

* the accession number will be preserved

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* the accession number will be preserved

* 22989 contig of 22988 bp in length

* 22989 109379: contig of 86391 bp in length

* 109380 154579: contig of 45200 bp in length

* 109380 154579: contig of 45200 bp in length

* 154580 15626: contig of 1647 bp in length

* 156227 166663: contig of 10437 bp in length

* 156227 166663: contig of 10437 bp in length

* 156227 166663: contig of 10437 bp in length

* Location/Qualifiers
Submitted (05-JUN-1999) Center for Human Genome Studies, DOE Genome Institute, Los Alamos National Laboratory, MS M888, I Alamos, NM 87545, USA
*NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L., Bryant,J., Tesmer,J., Melncke,L., Longmire,J., White,S., Tatum Campbell,C., Rawcett,J., Maltbie,M., Bussod,M., Sutherland,R.,
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1 (bases 1 to 16663)

Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D.,
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/db_xref="taxon:9606"
/clone="327F22"
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Pred. No. 3.9e-46;
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16 clone 327F22, WORKING DRAFT SEQUENCE, 5
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                                                                                                                                                                                                                                                                                                                                                                                             AC002429 23405
Human BAC clone (
AC002429
                                                                                                Submitted (19-AUG-1997)
University, 4444 Forest
SUBMITTED BY:
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 234053) Graves, T. Duckels, G and Hawkins, M. The sequence of H. sapiens BAC clone GS200K05 Unpublished (1997)
                                              Genome Sequencing Center
Department of Genetics
Washington University
                                                                                                                                                                    2 (bases 1 to 234053) Waterston, R.
mailto:sapiens@watson.wustl.edu
                St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
                                                                                                                                                       Direct Submission
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:lone GS200K05
                                                                                                                   Department of Genetics, Washington Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                                                                                                                                                                                                                                             DNA
5 from 7g21-g22,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send mailto:egreen@nhgri.nih

SOURCE INFORMATION: This clone is from the first BAC library from Genome (http://www.genomesystems.com). Systems,

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FEATURES
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Actual start of this clone is at base position 1 of 1 GS200K05;
actual end is at 234053 of GS200K05. The orientation of this clone is unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell line: lymphoblastoid Haplotypes: two VECTOR: pBeloBAC Selection: chloramphenicol
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                                                                                                           /rpt_family="L1"
complement(16228.
/rpt_family="ALU"
17447...17474
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complement(11288. .11342)
/rpt_family="L1"
  complement(20349.
/rpt_family="ALU"
complement(20398.
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/chromosome="7"
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43720. .43753
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complement(53772. .53879)
/rpt_family="L1"
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RESULT
AC007160
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                                                                                                                                                                         on Apr 7, 1999 this sequence version replaced gi:4508163.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                  Submitted (24-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Mo 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 142178)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of Homo sapiens clone
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       39502
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       9
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/rpt_family="L1"
                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                           Location/Qualifiers
 :lone="DJ0146I03"
33809 c 32673 g
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49152: gap of unknown length
142178: contig of 93026 bp in length
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Pred. No. 7.6e-46;
0; Mismatches 57
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Best Local Similarity 84.8%;
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                                                                                                                                                                                                                                                  Overlapping Sequences: 5': UWGC:djs77
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                  Double stranded (DS) coverage:
                                                                                                                                                                                                                       5': UWGC:ajs//
3': UWGC:mapping in progress
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                                                                                 Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                     University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Kerry Bubb (kbubb@u.washington.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 17975)
Iadonato,S.P., Yu,J., Wong,G.K.-S., Magness,C.L., Green,E.D., Green,P. and Olson,M.V.
Large-scale MCD Mapping and Sequencing of Human Chromosome 7 Unpublished (1999)
2. (bases 1 to 179757)
Bubb,K.D. and Desmarais,C.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-MAR-1999) Human Genome Center, University Washington, Box 352145, Seattle, WA 98195, USA
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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Pred. No. 8.1e-46;
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7p14-15,
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repear	8619.00	8708.00	3630.00	3666.00	2827.00	2816.00
י פטפפר ר	5023.00	5045.00	1024.00	1041.00	2913.00	2935.00
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repeat	737.00	748.00	1648.00	1659.00	5201.00	5276.00
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repear	2029.00	2016.00	8656.00	8690.00	5685.00	5679.00
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Source	999.00	1002.00	799.00	777.00	2589.00	2616.00
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	18.	527.00	7370.00	7389.00	1047.00	1068.00
	4995.00	5045.00	3354.00	3319.00	1208.00	1221.00
	2233.00	2230.00	1958.00	2020.00	4054.00	4040.00
	1786.00	1772.00	3619.00	3666.00	3.0	2421.00
	55	15887.00	2671.00	2717.00	540.00	542.00
	25	958.00	5	6542.00	2247.00	2260.00
	0.0	2016.00	2724.00	2717.00	9214.00	9301.00
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e d	Uniquely order	d values. (ed lines. Nsii	gredicted d predicted ed by dash RI	mental and mental and contact	the experi t groups ar bglii	between the expo fragment groups BglII
	ragments with sequence-predicted iragments is given below. Small fragments below a variable cutoff (approximately 400-600) are not resolved in the fingerprint and hence do not appear to the table made are affected to the decrease.	gments is in the second hence do	dicted iraciable cuto	low a var	gments be	ragments
	mplete Digest y derived dige	ultiple Co erimentall	dated by M	: been valion omparison o	alidation ence has nting. Co	Sequence Validation: This sequence has be fingerprinting. Com
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1482.00	1835.00 1532.00 1437.00	5678.00 17311.00 2655.00	1538.00 1766.00 3699.00	531.00 791.00 643.00

Unmatched fragments are due to vector-containing sequences. We expect 3, 1 and 1-2 such fragments in the BgIII, ECORI, and NsII enzyme domains, respectively. The sum of these fragments can be calculated from the sequence of the BAC clone and, in this clone, should be 26,152bp, 9,439bp, and 25,563bp for the three enzyme domains.

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JOURNAL
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KEYWORDS
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                                                                             Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                         2 (bases 1 to 134578)
Waterston, R.H.
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                              HTGS_PHASE1.
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/rpt_family="MSTAR"

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/rpt_family="Alu"

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е DJ020B21,
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Pred. No. 3.3e-45;
0; Mismatches 50;
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Direct Submission
Submitted (11-SEP-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA On May 12, 1999 this sequence version replaced gi:4757680.
* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 220000)
Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M.
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/db_xref="taxon:9606"
/clone="DJ020B21"
a 34383 c 33834 g 3383.
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Pred. No. 5.5e-45;
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                                                                                                  Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.
                        94071041
AL031775.1 GI:4071041
                                                                                 and putative CpG
AL031775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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119361
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         CpG island; KIAA0319; Y63D3A.4
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/db_xref="taxon:9606"
/chromosome="4"
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                                                                                                                                                                               102200 bp UNA Clone 30M3
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3: contig of 1203 bp in length
9: gap of unknown length
9: contig of 3870 bp in length
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9: contig of 3382 bp in length
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9: contig of 3382 bp in length
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Pred. No. 5.8e-45;
D; Mismatches 60;
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This sequence is the entire insert of clone 30M3.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was generated from part of bacterial clone contigs human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chf 1000 the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (05-JAN-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Aluo repeat: matches 1. 3467. .3763
/note="match: ESTs AA259531 AA289775 N50863 AA806198 AA931077 AA830274 AI199746 AA912273 AI081164 AG1288433 AA604069 AA772465 AA876363 AA52552 AI141796 AA59167 AA665259 AA289775 AA259531 AA731057 AA290469 D20450 AA517053 AA6669103 AA974142 AA903560 AI083595 AI187615 AI041875 AI1243439 N45220 R75494 AA798467 AA798167 AA798163 AA6591228 AA6653774 AA840219 AA041897 D77719 AA6653774 AA840219 AA041897 D77719 AA6653774 AA840219 AA041897 D77719
                                                                                                                                                                                                            4799. .4952

/note="MER3 repeat: matches 3. .154 of consensus"

Join(5119. .5233,7768. .9169)
                                                                                                                                                                                                                                                                                                                                                              /note="AluSp repeat: matches 1.
complement(3650, .4203)
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/note="FLAM_C repeat: matches 1. .126 of
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/note="AluSc repeat: matches 1.
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/clone_lib="RPCI1"
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/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 53.
                                                                                                                                                                                                                                                                                                                                        /note-"match: GSS B63434"
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                                                                                                                                                                                                                                                                                                                                                     11907. .12055
// Inote="MLTIA1 repeat: matches 146. .310 of consensus" complement(join(12316. .12571,15963. .>16147))
// Gene="dJ30M3.1"
// Inote="match: ESTS AA522110 AA207689 AA819653 AA928745
// Inote="match: ESTS AA522110 AA207689 AA819653 AA928745
// Inote="match: ESTS AA522110 AA207689 AA819653 AA928745
// Inote="match: ESTS AA522110 AA207689 AA812163 AA522456
// Inote="match: ESTS AA522110 AA207689 AA812163 AA522456
// Inote="match: ESTS AA522110 AA207689 AA812163 AA3228745
// Inote="match: ESTS AA522110 AA207689 AA822110 AA207689 AA8228745
// Inote="match: ESTS AA522110 AA207689 AA822110 AA207689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9439. .9621
/note="MIR repeat: matches 8. .256 of consensus"
9691. .9798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluJo repeat: matches 5..296 of consensus" 6740. .6878
/note="Min repeat: matches 69..207 of consensus" 7106. .7400
                                                                                                                                                                                             /evidence=not_experimental protein similar to (predicted) product="dJ30M3.1 (novel protein similar to (predicted) plant, worm, yeast and archaea bacterial proteins)" complement(12316) complement(12316) /gene="dJ30M3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:4210352"
/translation="AKFEFHHGDYEKQFLHVLSRKDKTGIVVNNPNQSVFLFIDRQHL
QTPKNKATIFKLCSICLYLPQBQLTHWAVGTIEDHLRPYMPE"
complement(join(12415. .12571,15963. .>16147))
/gene="dJ30M3.1"
                                                                complement(12316. .16147)
/gene="dJ30M3.1"
complement(12331. .12336)
/gene="dJ30M3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Alusx repeat: matches 1. .287 of consensus"
11907. .12055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11469. .11619
/note="MLT1A1 repeat: matches 1.
11620. .11906
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10855. .11115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="23 copies 2 mer tt 78% conserved"
9092. .9129
/note="19 copies 2 mer aa 82% conserved"
}124. .9129
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revidence=not_experimental
/product="d330M3.2 (novel protein)"
5119. .9169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1MC4 repeat: matches 7851. .7977 of consensus"
10020. .10149
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/gene="dJ30M3.2"
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                                                                                                                                                                                            TGGTGAAATCCTGTCTGTACTAAAAATACAAAAGTTAGCTGGATATGGTGGCAGGCGCCT 1318
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                                     TTGAAGTGAGTTGAGATCACACCACTATACTCCAGCTGGGGCAACAGAGTAAGACTCTGT 1438
                                                                                                          GTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGG 1378
                                                                                                                                                                                                                                                        TGGGAGGCTGAGGTGGGCAGATCACTTAAGGTCAGGAGTTCGAGGCCAGTCTGGCCAATA 83705
                                                                                                                                                                                                                                                                                   TGGGAGGC-GAGGCAGGCAGATCACTTGAGGTAAGGAGTTCAAGACCAGCCTGGCCAAAA 1258
TTGCAGTGAGCTGAGATTGCACCACTGTACTCCAGTCTGGGTGACAGAGCAAGATTCTGT 83525
                                                                               GTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGGCGGAGG 83585
                                                                                                                                                                    TGGTGAAACCCTTTCTCTATTAAAAATAAAAAATTAGCCAGGTATGGTGACATGCGCCT 83645
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/note="hlusx repeat: matches 24.

complement(20331... .20463)

/note="match: GSS B74972"

21207. .21337
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/note="Aluxa8 repeat: matches 1.

15123. 15387

/note="Aluxx repeat: matches 30.

15514. 15624
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/protein_id="CAA21139.1"
/db_xref="pID:e1373175"
/db_xref="pID:e1373175"
/db_xref="pID:e1373175"
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P95914; supported by GENSCAN and FGENES"
/codon_start=1
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/note="Alusx repeat: matches 6.
19037. 19404
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19504. .19639
/note="MIR repeat: matches 88.
20030. .20303
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16957. 17250
/note="AluSg repeat: matches 1.
17526. 17589
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/translation="ITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVDNISTMA
/translation="ITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVDNISTMA
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Pred. No. 6.7e-45;
0; Mismatches 84;
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E to 80507)

E (bases 1 to 80507)

S Muzny, D., Arenson, A.D., Adams, C., Bunac, C., Carvelli, K., Chang, J., Chacko, J., Chen, J., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Hernandez, J., Jackson, L., Jin, S., Kampal, R., Karpathy, S., Kovar, C., Lau, S., Leal, B., Lee, E., Li, Y., Lichtarge, O., Liu, W., Logan, O., Lu, J., Ly, T., Marondel, I., Martinez, C., Merscher, S., Montgomery, K., Ogwal, G., Perez, L., Rashid, N.D., Renault, B., Rowland, K., Savage, L., Scherer, S.E., Shen, H., Simon, M., Stovall, K., Timms, K.M., Todd, J., Vo, Q., Williamson, A., Worley, K.C., Yu, W., Kucherlapati, R., Nelson, D. and Gibbs, R.A.
                                                                                                                                                                          Submitted (17-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 31, 1998 this sequence version replaced g1:3242678.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 80507)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (31-JUL-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 80507)
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Direct Submission
                                                                             Sequence similarities were identified using
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HOMO SAPIENS 12q24.2 PAC RPCI1-128M12 (ROSWELL PARK CANCER INSTITUTE HUMAN PAC library) complete sequence.
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Location/Qualifiers
                                                                                                                                         /rpt_family="MER3"
complement(12988. 13296)
/rpt_family="AluSp"
complement(13299. 13631)
/rpt_family="AluSp"
..__amily="(CA)n"
complement(14076. .14283.
                                                                                                                                                                                                                                                                               complement(11421 ...11516)
/rpt_family="AluJo_FRAM"
complement(11526 ...11644)
/rpt_family="(TA)n"
12156 ...12452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6721, .69ap,
/rpt_family="",
compression
                                                                         complement(13639..13726)
/rpt_family="MIR"
complement(13819..13874)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family-"(GAAA)n"
763. .1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="(GGAA)n"
666. 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(10941. .10998)
/rpt_family="(CA)n"
11051. .11338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(7363. .7392)
/rpt_family="AT_rich"
10233. .10531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Alusx"
complement(4547. .4855)
/rpt_family="Alux"
5542. .5836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Unknown"
/note="Contains two Unigene clusters. F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Alusx"
complement(join(2358. .2887,3646. .3719,4946. .5090,7752. .7890,8220. .8254,38145. .38168,64167. .64298))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name="G19891"
/note="Genethon pending:RH10692, A002B25, STS32769,
GDB:4563466, Chr. 12-12, Homo Sapiens"
/db_xref="dbSTS:32769"
                                                                                                                  /rpt_family="Alux"
complement/12677
                                                                                                                                                                                                                                                                                                                                                                                       complement(11339.
/rpt_family="(TA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alusx"
complement/667'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2391. .2559
/gene="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Overlaps with bases 139060 to 139166 in note="Region: Overlap with AC003029."
                                                                                                                                                                                                                                                            /rpt_family-"Alusc"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family='
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alusx"
complement/730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alusg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accession numbers are za72d06.rl."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="12q24.2"
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/db_xref-"taxon:9606"
/clone-"RPCI1-120M12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _family="Alusc"
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Representative , and clone

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Best Local Similarity
Matches 272; Conserv
                                                1203 GAGGCG-AGGCAGGCAGATCACTTGAGGTAAGGAGTTCAAGACCAGCCTGGCCAAAATGG 1261
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complement(16845. 17079)
/rpt_family="MER47A"
17137. 17231
                                                                                                                                                                                                                                                          /rpt_family="LTR22"
complement(26739. .27076)
/rpt_family="MER7A"
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complement(14592. .14896)
/rpt_family="AluSq"
15215. .15420
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23338.
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23008
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21535.
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21235
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15576. .15984
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                                                                                                                                                                         Score 234.6; DB 11; Length 80507; Pred. No. 6.6e-45; 0; Mismatches 44; Indels 1;
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        4120
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ORGANISM
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AC004971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTGAGTTGAGATCACACCACTATACTCCAGCTGGGGCAACAGAGTAAGACTCTGTCTC 1441
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2 (bases 1) to 188477)
2 (bases 1) to 188477)
2 (bases 2) to 2 (bases 2) to 2 (bases 3) to 2 (bases 4) to 2 (ba
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188477)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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HTG; HTGS_PHASE1.
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source
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                                                                                                                                                                                                                                                                                                                                                                                                           86861 GAGCCGAGATGCCGCCACTGCACTCCAGCCTGGGCAAGAGAGTGAGACCCCTGTCTCAAAA 86920
                                                                                                                                                                                                                                                    86801 CAGCTACTTGGAAGGCTGAGGCAGGAGAATCGCTTGAGCCTGGGAAGTGGAGGTTGTGGT 86860
                                                                                                                                                                                                                                                                                                                                  86741 ACCCTGTCTCTACTAAAAATACAAAAATTATCTGGACGTGGTGGCGGGCACCTGTAATCC 86800
                                                                                             1446 AAAAAAAAAAAAA 1458
||||||||||||
86921 AAAAAAAAAAAAA 8693:
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50114: contig of 9684 bp in length
50133: gap of unknown length
67886: contig of 17753 bp in length
67905: gap of unknown length
84164: contig of 16259 bp in length
84183: gap of unknown length
105583: contig of 21400 bp in length
105602: gap of unknown length
128036: contig of 22434 bp in length
128036: contig of 2767 bp in length
188122: contig of 57067 bp in length
185140: gap of unknown length
185140: gap of unknown length
186840: contig of 1700 bp in length
186877: contig of 1619 bp in length
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1459; Conservative 0; Mismatches
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W09837093-A2.
27-AUG-1998.
27-FEB-1998. U03492.
09-FEB-1999. U5-020956.
25-FEB-1997. US-806099.
01-AUG-1997. US-904804.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI, 98-609886/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 106; 130pg; English.

The present sequence is a new DNA which encodes an immunogenic portiof a prostate tumour protein. The encoded immunogen, or the DNA itsection be used as a vaccine for the treatment of prostate cancer The E was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.

Sequence 1459 BP; 427 A; 328 C; 406 G; 295 T;
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27-AUG-1998.
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V61250 standard; cDNA; 1265
V61250;
06-JAN-1999 (first entry)
cDNA sequence of prostate to
Prostate; cancer; tumour; v6
Homo sapiens.
W09837093-A2.
27-AUG-1998.
25-FEB-1998; U03492.
09-FEB-1998; US-020956.
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PR 25-FEB-1997; US-806596.

PR (CORI-) CONIXA CORP.

PI Dillon DC, Xu J;

PR Novel human prostate specific tumour protein and fragments - useful protecting and treating prostate cancers

Pr Novel human prostate specific tumour protein and fragments - useful pr for detecting and treating prostate cancers

PS Claim 1; Page 113-114; 141pp; English.

CC This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as canced by this sequence). An antibody which binds to an immunogenic cortion of the prostate protein, and the method can be used to detect, consolitor progression of, or treat prostate cancers. The antibody may calso be conjugated to a therapeutic agent for use in therapy of prostate cancers.

SO Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T;
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nilarity 98.4%;
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Pred. No. 4.4e-95;
0; Mismatches 8
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tumour clone P703 splice variant vaccine; immunogen; clone; ss.

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01-AUG-1997; (
(CORI-) CORIX/
Dillon DC, xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 105-106; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic port. of a prostate tumour protein. The encoded immunogen, or the DNA its, can be used as a vaccine for the treatment of prostate cancer. The was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.
                                              11-SEP-1998 (first entry)
Homo sapiens Tub Interactor (hTI-1) gene.
serine protease; tub interactor; treatment; obesity; cachexia; anorexia nervosa; diabetes; cell cycle progression; apoptosis; neurodegenerative disease; Alzheiner; disease; drug screening; Parkinson's disease; Huntington's chorea; detection; diagnosis; amylotrophic lateral sclerosis; spinocerebellar degeneration; s:
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WPI; 98-609886/51.
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Pred. No. 4.4e-95;
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26-MAR-1998.
05-SEP-1997; U15627.
21-JUL-1997; US-8973.
17-SEP-1996; US-7150.
(MILL-) MILLENNIUM PEIRAGA PR, Gimeno CJ
WPI: 98-217246/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  weight disorders, e.g. obesity, cachexia or anorexia nervosa, or a related disorder such as diabetes. The products can also be used to modulate cell cycle progression and apoptosis. They can be used for treating neurodegenerative diseases which are characterised by apoptosis, including Alzheimer's disease, Parkinson's disease, Huntington's chorea, amylotrophic lateral sclerosis or spinocerebellar degenerations. The products can also be used for detection, diagnosis and drug screening.

Sequence 1386 BP; 318 A; 490 C; 321 G; 249 T;
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The sequence is that of the Tub Interactor gene hTI-1 wl codes for a putative serine protease. TI genes function in biochemical pathways involved in weight control and related disorders. The products can be used for treatile telegraphic treatments of the products can be used for treatments.
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Pred. No. 2.3e-63;
0; Mismatches 3
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Matches 422; Conserv
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25-FEB-1998: U03690.
99-FEB-1998: US-904809.
25-FEB-1997: US-806596.
01-AUG-1997: US-904809.
(CCRI-) CORIXA CORP.
Dillon DC, Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers
Claim 1, Page 112; 141pp; English.
This sequence represents a human prostate tumour specific gene, and car be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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WPI; 98-480805/41.
P-PSDB; W69387.
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V58644;
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                                GAGGTCTGCANTAAGCTCTATGACCCGCTGTACCACCCCANCATGTTCTGCGCCGGCGGA
                                                                                                                                                               CGCGGGAACTCTTGCCTCGTTTCTGGCTGGGGTCTGCTGGCGAAC-------
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                       GAGGTCTGCAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGA
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gene; human; pr
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Pred. No. 2.2e-63;
0; Mismatches 3
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Best Local :
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Homo saptens.
W09837033-A2.
27-AUG-1998.
U03492.
25-FEB-1998; US-020956.
25-FEB-1997; US-806099.
C1-AUG-1997; US-904804.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI, 98-60988/51.
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V61249;
06-JAN-1999 (1
CDNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 104; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.

Sequence 1248 BP; 288 A; 424 C; 303 G; 228 T;
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22; Conservative
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tumour;
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27-AUG-1998: U03690.
25-FEB-1998: US-904809.
25-FEB-1997: US-806596.
01-AUG-1997: US-904809.
(CORI-) CORIXA CORP.
D111on DC, Xu J;
WPI: 98-480805/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V58647 standard; cDNA; 1167
V58647;
08-DEC-1998 (first entry)
Prostate tumour specific generostate tumour specific gentherapy; ss
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This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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Local Similarity
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                         CGTGCTGCAGTGCGTGAACGTGTCGGTGGTGTCTGANGAGGTCTGCANTAAGCTCTATGA
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                                                                                                           GGTCCTCTGCCCAGTCGCGGGGGCTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTAC
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Pred. No. 1.8e
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Best Local Similarity
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09-FEB-1998; US-020956.

25-FEB-1997; US-806099.

01-AUG-1997; US-904804.

(CORI-) CORIXA CORP.

D1110 DC, Xu J;

WPI; 98-609886/51.

P-PSDB; W71782.
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WO9837093-A2.
27-AUG-1998.
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The present sequence is a new DNA which encodes an immunogenic por of a prostate tumour protein. The encoded immunogen, or the DNA is can be used as a vaccine for the treatment of prostate cancer. The can be used as a vaccine for the treatment of prostate cancer. The was identified by analysis of a subtracted cDNA library obtained by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtracting a prostate tumour cDNA expression library with a tissue cDNA library.

Sequence 1167 BP; 242 A; 400 C; 287 G; 222 T;
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V61252;
06-JAN-1999 (first entry)
cDNA sequence of prostate
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                       CCCGCTGTACCACCCCANCATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCCTG
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Best Local Similarity
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31-OCT-1997. U20051.
05-NOV-1996; US-744026.
(INCY-) INCYTE PHARM INC.
Bandman O. Goll SK;
                                                                                                                                                                                                                                                                                                                    Claim 5; Fig 1A-C; 68pp; English.

This DNA encodes a human prostate-specific kallikrein (HPSK). A host cell containing an expression vector comprising the HPSK nucleic acid sequence can be used to produce the protein recombinantly. The HPSK products can be used for the diagnosis of conditions or diseases associated with expression of HPSK such as prostate carcinoma and benign prostate hyperplasia. Agonists and antagonists which specifically bind to HPSK and modulate its activity can be used for the preparation of treatment of such conditions or diseases. The products can also be used for detection and drug screening, especially for the detection of prostate-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-1998 (first entry)
Human prostate-specific kallikrein (HPSK) encoding DNA.
Prostate-specific kallikrein; HPSK; prostate carcinoma;
benign prostate hyperplasia; diagnosis; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V37495
V37495;
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|||||
489 CAACG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated prostate-specific kallikrein - used to develop for diagnosis and treatment of, e.g. prostate carcinoma or i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 98-286933/25.
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                                                                                   CCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCCTCGTTT
                                                                                                                  CCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
            GGTCCTCTGCCCAGTCGCGGGGGGCTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTAC
                                                      CTGGCTGGGGTCTGCCGGAACGGTGAGCTCACGGGTGTGTCTGCCCCTCTTCAAGGA
                                                                         ACATCCGGAGNATCAGCATTGNTTCGCAGTGCCCTACCGCGGGGAACTTTTGCCTCGTTT
                                                                                                                                                              AGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCCAGAGTACAACAGAC
                                                                                                                                                                                   AGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCCAGAGTACAACAGAC
                                                                                                                                                                                                                                                   389;
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871 BP;
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/transl_except= (pos:412.
/transl_except= (pos:424.
/product= "HPSK protein"
/note= "Xaa = unknown"
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31. .777
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Pred. No. 2.7e-55
D; Mismatches 1
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aa:Xaa)
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                                                                                                                  Query Match
Best Local
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168

ACGGCACCCAGAGTACAACAGACCCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGGA 181

62

108

N

Similarity

Score 289.4; Pred. No. 7.

В <u>ــر</u>

Mismatches

).6e-55; ies 2;

Indels Length 402;

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Gaps

0

Conservative

GTCAGCCGCACACTGTTTCCAGAAGTGAGTGCAGAGCTCCTACACCATCGGGCTGGGCCT

GTCAGCCGCACACTGTTTCCCAGAAGTGAGTKCAGAGCTCCTACACCATCGGGCTGGGCCT

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CC X41094 to X41347 represent 5' expressed sequence tags (ESTs) for human CC secreted proteins, and encode the proteins given in x12261 to x12514, CC respectively. The proteins given represent the signal peptide and an CC N-terminal fragment of a secreted protein The nucleic acid sequences CC can be used for producing secreted human gene products. They can also CC be used to develop products for diagnosis and therapy. The proteins CC obtained may have cytokine activity, cell proliferation/differentiation CC activity, haematopoiesis regulating activity, tissue growth regulating CC activity, reproductive hormone regulating activity, chemotactic/ CC ligand activity, haemostatic and thromobytic activity, receptor/ CC chemokinetic activity, haemostatic and thromobytic activity, receptor/ CC or other activity, anti-inflammatory activity, tumour inhibition activity and chromosome mapping procedures. The sequences can also be used for Obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or cimporting a polypeptide into a cell.

Sequence 402 BP; 80 A; 125 C; 121 G; 75 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein 5° EST SEQ ID NO:58.

Human; secreted protein; EST; expressed sequence tag; diagnosis;
forensic; gene therapy; chromosome mapping; signal peptide;
upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopolesis regulation; tissue growth regulation;
reproductive hormone regulation; chemotractic; chemokinetic; haemostatic;
thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids encoding human secreted proteins - obtained front interior property in the protein of the control protein of the control protein of the colon tissue kidney, lung, umbilical cord, placenta and colon tissue claim 1; page 205; 824pp; English.

X41094 to X41347 represent 5, expressed sequence tags (ESTs) for X41094 to X41347 represent 5, expressed sequence tags (ESTs) for X41094 to X41347 represent 5, expressed sequence tags (ESTs) for X41094 to X41347 represent 5, expressed sequence tags (ESTs)
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W09906548-A2.
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Duclert A, Dumas Milne Edwards
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01-AUG-1997; US-905135.
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X41114;
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RESULT
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Best Local Similarity
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27-AUG-1998: U03690.
25-FEB-1998: US-904809.
09-FEB-1997: US-806596.
01-AUG-1997: US-904809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI; 98-480805/41.
P-PSDB; W69389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate tumour :
Prostate tumour :
therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                     for detecting and treating prostate cancers

Claim 1; Page 116-117; 141pp; English.

This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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08-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human prostate specific tumour protein and fragments
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            CIGCTGGGGTCTGCTGGCGAACGAIG
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                                                                                                                                                                                      AGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCCAGAGTACAACAGAC 144
                                                                                                                                                                                                                            ACTGTTTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAG 157
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c gene; human,
                                                                                                                                                                                                                                                                              ; Score 257.4; ; Pred. No. 9.6e 0; Mismatches
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ID T18325 standard; DNA; 24026
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Best Local S
Matches 261
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WO9837093-A2.
27-AUG-1998.
                                                                                                                                                                                                                                                    05-JUN-1996 (first entry)
BRCA1, human breast and ovarian cancer predisposing gene.
BRCA1; breast cancer; ovary cancer; predisposing gene;
BRCA1; breast cancer; ovary cancer; predisposing gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer Claim 3; Page 108-109; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic po of a prostate tumour protein. The encoded immunogen, or the DNA i can be used as a vaccine for the treatment of prostate cancer. The was identified by analysis of a subtracted cDNA library with a norm tissue cDNA library.

Sequence 1119 BP; 248 A; 305 C; 282 G; 284 T;
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09-FEB-1998; US-020956.
25-FEB-1997; US-806099.
01-AUG-1997; US-904804.
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Dillon DC, Xu J;
WPI; 98-609886/51.
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06-JAN-1999 (first entry)
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56. .155
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156. .1512
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1513. .1611
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Best Local Similarity 87.0
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07-OCT-1996 (first entry)
Mutated BRCA1 genomic sequence from sample set MSKCC family 19921.
Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;
Mutibody production; germline alteration; probe; lesion neoplasia; human;
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07-OCT-1996
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D; Mismatches 38;
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356. .1512
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365. .6571
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814. .3902
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925. .1937
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Best Local Similarity 87.0%;
Matches 260; Conservative
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Pred. No. 1.3e-40;
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Search completed: September 28, 1999, 12:28:26 Job time: 5326 sec

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Result

Pred. No. is the number of x score greater than or equal and is derived by analysis of

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Searched: Scoring table: Sequence:

Title: Perfect score:

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GenCore version 4.5 Copyright (c) 1993 - 1998 Comp

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US-08-744-026-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Patent No. 5785148
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL PROSTATE-SPECIFIC
TITLE OF INVENTION: KALLIKREIN
                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                   Query Match
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Versio
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                       LENGTH: 871 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY:
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MEDIUM TYPE: Diskett
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ADDRESSEE: INCYTE PHARMACEUTICALS,
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CITY: Palo Alto
STATE: CA
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89; Conservative
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US-08-080-255-6

PCT-US93-05857-6

US-07-914-281-5

US-08-93-246-5

US-08-068-945A-1

US-08-273-411-2
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Pred. No. 1.
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Patent No. 5693473; General INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldar APPLICANT:
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                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Shattuck-EAULING APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                            APPLICATION NUMBER: US/08/480,784 FILING DATE: CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/308,104 FILING DATE: 16-SEP-1994 RIOR_APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACG 625
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1201 New York Avenue, N.W., Suite 1000
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Shattuck-Eidens, Donna
Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                                                        USA
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US-08-480-784-20
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Best Local Similarity 87.0
Matches 260; Conservative
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INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY,AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1401
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APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian
TITLE OF INVENTION: Susceptibility Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1281
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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ANTI-SENSE: NO
STREET:
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                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGATCACAC 1400
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       Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skolnick, Mark I
Goldgar, David I
Miki, Yoshio
                                    E: Venable, Baetjer, Howard & Civiletti, 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                             Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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COUNTRY: U ZIP: 20005

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APPLICATION NUMBER: US 0 FILING DATE: 24-MAR-1995 PRIOR APPLICATION DATA:

CLASSIFICATION: 435 PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

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NFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   1221 CACTTGAGGTAAGGAGTTCAAGACCAGCCTGGCCAAAATGGTGAAATCCTGTCCTGTACTA 1280
                                                                                                                                                                                                                                                                                                                                               1162 GCTGGGCAGGGTGGCTCATGCCTGTAATCCCCAGCACTTTGGGAGGC-GAGGCAGGAGAT 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
                                                                                                                                                                                           1281 AAAATACAAAAGTTAGCTGGATATGGTGGCAGCCGCTGTAATCCCAGCTACTTGGGAGG 1340
                                          5683 CACTTGAGGTCATGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCCATCTCTACTA 5624
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                       CTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGATCACAC 1400
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Pred. No. 9.5e-48;
0; Mismatches 38
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US-08-487-002-20/
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                                                                          Query Match
Best Local Similarity
Matches 260; Conserv
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TELEPHONE: 202-962-4810
TELEPHANE: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
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                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Homo
                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: 1
5743 GCTGGGCACGGTGGCTCAAGCCTGTAATTCCAGCACTTTGGGAGGCTGAGGCGGGTGGAC 5684
                       1162 GCTGGGCAGGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGC-GAGGCAGCAGAT 1220
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APPLICATION NUMBER:
FILING DATE: 12-AUG-
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FILING DATE: 29-NOV-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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APPLICATION NUMBER: US 0:
FILING DATE: 24-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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CITY: Washington
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APPLICANT: Durocher, Francine
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ihnen, Jeffrey REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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Simard, Jacques
                                                                            Conservative
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12-AUG-1994
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16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US 08/348,824
29-NOV-1994
                                                                                                                                                                                                                                                                                                    double
                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                       15.5%;
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                                                                          Score 226.2; DB 2
Pred. No. 9.5e-48;
0; Mismatches 38
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Gaps

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Query Match
Best Local Similarity
Matches 260; Conserv

Conservative

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; ORIGINAL SOURCE: ; ORGANISM: Hom US-08-483-553-20

Homo sapiens

MOLECULE TYPE: HYPOTHETICAL: N ANTI-SENSE: NO

TYPE: nucleic acid
STRANDEDNESS: double

linear 8

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                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/ACENT INFORMATION:
NAME: Ihnen, Jeffrey L.
                                                                                                                                                                                            APPLICATION NUMBER: US/08/483,554B FILING DATE: 07-TUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-MOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
ETILING DATE: 16-SEP-1994
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer TITLE OF INVENTION: Susceptibility Gene NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28 957
REFERENCE/DOCKET NUMBER: 241
TELECOMMUNICATION INFORMATION:
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Tavtigian, Sean V.
Wiseman, Roger W.
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Goldgar, David E.
Miki, Yoshio
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                        24884-109347
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,011B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 260; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 6769 base pairs
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APPLICANT:
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti,
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                               TITLE OF INVENTION: 17q-Linked Breast and TITLE OF INVENTION: Susceptibility Gene
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                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                STATE: DC
COUNTRY: US
ZIP: 20005
                                                                                                                                                                     STREET: 1201 New CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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Wiseman, Roger W.
Futreal, P. Andrew
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Shattuck-Eidens, Do
Shattuck-Eidens, Do
                                                                                                                                             USA
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Goldgar, David
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Pred. No. 9.5e-48;
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: Sequence 20, Application PC/TUS9510202

: GENERAL INFORMATION:
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Best Local Similarity
Matches 260; Conserv
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Eni, Mitsuru
APPLICANT: Nakamura, Yusuke
APPLICANT: Nakamura, Francine
TITLE OF INVENTION: In Vivo Mutations
TITLE OF INVENTION: Susceptibility Ger
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[NFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347-09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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ORGANISM: Hom
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FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/300,266 FILING DATE: 02-SEP-1994 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 24-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/308,104 FILING DATE: 16-SEP-1994
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                                                                                                                                                                                                                                CTGAGGCAGGAGTATGGCTTCAACCTGGGAGGCGAGACGTTGCGGAGAGGTGAGATCACAC
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In Vivo Mutations and Polymorphisms in the 17q-Linked Breast and Ovarian Cancer Susceptibility Gene
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Pred. No. 9.5e-48;
0; Mismatches 38; Indels 1;
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MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO
PCT-US95-10202-20
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Best Local Similarity
Matches 260; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE_/OOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,95
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APPLICATION NUMBER: US 08/
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                           1162 GCTGGGCAGGGTGGCTCATGCCTGTAATCCCCAGCACTTTGGGAGGC-GAGGCAGGCAGAT 1220
                                                                                                                                          5743 GCTGGGCACGGTGGCTCAAGCCTGTAATTCCAGCACTTTGGGAGGCTGAGGCGGGTGGAC 5684
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APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS: Panable, Baetjer, Howard & Civiletti, LLP
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                         5683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
1341 CTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGATCACAC 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/10202
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                                                             AAAATACAAAAGTTAGCTGGATATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGG 1340
                                                                                                                CACTTGAGGTCATGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCCATCTCTACTA 5624
                                        AAAATACAAAAATTAGCCGGGTGTGGTGGCGCGCGCCTGTAGTCCCAGCTACTAGAGAGG 5564
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12-AUG-1994
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                                                                                                                                                                                                                                                                                Score 226.2; DB 5
Pred. No. 9.5e-48;
0; Mismatches 38
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                                                                                                                                                                                                                                                                                                                        DB 5;
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                                                                                                                                                                                                                                           TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17g-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US OF FILING DATE: 29-NOV-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 24-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 00 FILING DATE: 02-SEP-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 00 APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-
PRIOR APPLICATION DATA:
MOLECULE TYPE:
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                       nucleic acid
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                                                                                                                                                     6769 base pairs
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Goldgar, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US 08/289,221
12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US 08/409,305
24-MAR-1995
DNA (genomic)
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PCT-US95-10220-20/c
; Sequence 20, Application PC/TUS9510220
; GENERAL INFORMATION:
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Best Local Similarity
Matches 260; Conser
                                                                                                                                               STATE: DC
COUNTRY: USA
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10220
EILING DATE:
EILING DATE:
                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/409,305
EILING DATE: 24-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1341 CTGAGGCAGGAGATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGATCACAC 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                 STREET: 1201 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGGCAGGAGTATGGCTTCAACCTGGGAGGCCAGACGTTGCGGAGAGGTGAGATCACAC 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harshman, Neich
Shattuck-Eidens, Do
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   US 08/348,824
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Pred. No. 9.5e-48;
0; Mismatches 38
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FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0
FILING DATE: 16-SEP-1994

US 08-308,104

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 APPLICANT: Bergsma, Derk J.

APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/Uw2220
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                  Sequence 7, Application US/08451777A Patent No. 5789223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.5%;
Best Local Similarity 87.0%;
Matches 260; Conservative
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LENGTH: 6769 base pairs
TYPE: nucleic acid
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FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5623 AAAATACAAAATTAGCCGGGTGTGGGGGGGGGGGCGCTGTAGTGCCAGCTACTAGAGAGG 5564
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                            5683 CACTTGAGGTCATGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCCATCTCTACTA 5624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                  CTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGATCACAC 1400
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12-AUG-1994
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Pred. No. 9.5e-48;
N4 smatches 38;
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WESULT 11
US-08-451-778A-7/c
; Sequence 7, Application US/08451778A
; Patent No. 5β30649
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Best Local Similarity 85.3%; Pred. No. 5.7e-46;
Matches 256; Conservative 0; Mismatches 43
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FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Allssa M.
REGISTRATION NUMBER: 950268-1B
REFERENCE/DOCKET NUMBER: P50268-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pair
                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                        APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           5878
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1340 GCTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGATCACA 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: OC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                5938 AAAAATACAAAAGTTAGCCGGGCATCGTGGCAGGCGCCTGTAATCCCCAGCTACTCAGGAG 5879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1280 AAAAATACAAAAGTTAGCTGGATATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAG 1339
                                           STREET: 709 SWEUGIALL CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 610-2, 5090 TELEPHONE: 610-270-5090
COUNTRY: USA
ZIP: 19406-0939
                                     STATE:
                                                                       ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road/UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: do TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCCTGAGGTCAGGAGCTCGAGACCAGCCTGGCCAACATGGCGAAACCCCCGTCTCTACT 5939
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pennsylvania
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-451-778A-7
                                                                                                                                                                                                                                                                                                                                                                                     US-08-998-208-7/c
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08998208 Patent No. 5880105
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Best Local Similarity
Matches 256; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,778A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DAYA:
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
REGISTRATION NUMBER: 37,126
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1280 AAAAATACAAAAGTTAGCTGGATATGGTGGCAGGCGCCTGTAATCCCCAGCTACTTGGGAG 1339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: King of Prussia
STATE: Pennsylvania
                                                                                      COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                               ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road/UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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85.3%;
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Matches
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COUNTRY: USA
ZIP: 19406-0939
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V4
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 256; Conserv
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Version #1.30

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RESULT 13
PCT-US95-06743-7/c
; Sequence 7, Application PC/TUS9506743
; GENERAL INFORMATION:
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APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/UW2220
CITY: King of Prussia
STATE: Pennsylvania
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FILING DATE: 26-MAY-1995
APPLICATION UMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
REGISTRATION NUMBER: 37,126
REGISTRATION NUMBER: P50268-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
TELEFAX: 610-270-5990
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1280 AAAAATACAAAAGTTAGCTGGATATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: US/08/998,208
                                                                                                                                                                                                                                                                                                                                                                                                        1340 GCTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGATCACA 1399
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85.3%; Pred. No. 5.7e-46;
tive 0; Mismatches 43
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RESULT 14
US-08-370-975B-1
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Best Local Similarity 85.3%;
Matches 256; Conservative
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TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Maley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028 REFERENCE/DOCKET NUMBER: P50 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5024
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1161 GGCTGGGCAGGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGC-GAGGCAGGCAGA 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5998 TTGCCTGAGGTCAGGAGCTCGAGACCAGCCTGGCCAACATGGCGAAACCCCCGTCTCTACT 5939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1340 GCTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTTGAGATCACA 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                COUNTRY:
                                                                                                                                                                                 STREET: Clinton CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
   APPLICATION NUMBER:
                                                                                                                               14603
                                                                                                                                                                   New York
                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/US94/10825
US/08/370,975B
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Pred. No. 5.7e-46;
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                                      Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08370975B Patent No. 5622851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 261; Conserv
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Waley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Melner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2555 GGTCAGACCAAAAGCCAGAAGTGAGGCTGGGCACGATGGCCTCACGCCTGTAATCCCAACA 2614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1137 GGAAAAATCAAGACTCTACAAAGAGGCTGGGCAGGGTGGCTCATGCCTGTAATCCCAGCA 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2855 TGTCTCAAAAAACAAAACAAAAA 2877
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                                                                                                                    COUNTRY:
ZIP: 146
                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 26764 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Timian, Susan J
REGISTRATION NUMBER: :
SOFTWARE: Patentin Release #1.0, RRENT APPLICATION DATA:
                                                                                                                                                           STATE:
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                                                                                                                                                                                  CITY:
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: New York
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(716)263-1600
                                                                                                                                         USA
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Pred. No. 2.7e-44;
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                    Version #1.25
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APPLICATION NUMBER: US/08/370,975B
FILING DATE: 10-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20894/80
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1636
TELEFAX: (716)263-1636
TELEFAX: (716)263-1600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 4q35
US-08-370-975B-6
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Search completed: September 28, 1999, 11:33:47 Job time: 2107 sec
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                                                                                                                                                                                                                                                     1376 AGGTTGAAGTGAGATTGAGATCACACCACTATACTCCAGCTGGGGCAACAGAGTAAGACTC 1435
                                                                                                                                                                                         832 AGGTTGTAGTGAGCCAAGACTGCGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTC 891
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seq_documentation_block:

ID 042160 PRELIMINARY; PRT; 245 AA.

AC 042160;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

TRYPSINOGEN B2 PRECURSOR (FRAGMENT).
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US-09-030-606-173 x 042160 ...
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Quality:
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Ratio: 2.664
Percent Similarity: 64.898
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SEQUENCE
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NON_TER
SIGNAL
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ROACH J.C.;

Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF011901; AAB69657.1; -.

PFAM; PF00089; trypsin; 1.
                  404 GGTCCTCTGCCCAGTCGCGGGGGCTGACCCAGAGCTCTGCGTCCCAGGCA 453
                                                           145
                                                                                                                                                        110 TCCAGAACTCC.....TACACCATCGGGCTGGGCCTGCACAGTCTTGAG 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Cephalaspidomorphi;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 rAsnAlaTrpIleAlaGlnThrIleAlaAlaAsn
                                                                                                                                         129
                                                                                                                                                                                                                                      254 AGTIGGACGAATCCGIGICCGAGTCTGACACCATCCGGAGCATCAGCATT 303
                                                                                                                                                                                                                                                                                                                                                                                                                154 GCCGACCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACG 203
                                                                                                354 TCTGCTGGCGAACGGTGAGCTCACGGGTGTGTGTCTGCCCTCTTCAAGGA 403
                                                                                                                                                                                                                                                                                                                                                                         80 Val...ThrGluGlyThrGluGlnArgIleGlnAlaSerLysAlaIleAr 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 HisSerGlnProTrpGlnValSerLeuAsnIleGlyTyrHis...PheCy 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 CACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTG 59
                                                                                                                                     ProSerSerCysValGlyThrGlyValMetCysThrIleSerGlyTrpGl 145
                                                     1 1 1 POTENTIAL.
<1 13 POTENTIAL.
14 245 TRYPSIN B2.
245 AA; 26001 MW; 071872F0 CRC32;
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Gaps: 6
Percent Identity: 36.327
247
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146	GluThrGlnThrSerValGly	152
454		503
153	SerProAspValLeuMetCysValGlnAlaProValLeuSerAspThr	168
504	GACCCGCTGTACCACCCCAGCATGTTCTGCGC	553
169	SerCysArgAsnSerTyrProGlyAspIleThrAsnAsnMetIleCysLe 1	185
554		603
185	uGlyTyrLeuGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyP	202
604		653
202	roValValCysAsnGlyGlnLeuGlnGlyIleValSerTrpGlyArgGly	218
654	PAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATT	703
219	CysAlaLeuProAsnTyrProGlyValTyrThrLysValCysAsnTy	234
704	CACTGAGTGGATAGAGAAAACCGTCCAGGCCAGT 737	
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Perfect score:
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1265
1 GGCAGCCCGCACTCGC
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em_est7:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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KEYWORDS	VERSION	NID	ACCESSION	DEFINITION	LOCUS	AI557281	RESULT
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EST.	AI557281.1 GI:4489644	q4489644	AI557281	PT2.1_15_G12	AI557281		
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	448964			tumor2	77 bp		
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  GGTGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTT
                           GGTGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGACCCGCTGTACCACCCCCAGCATGTT 547
                                                                                                                                                                                                                                                                                                                                                             CCAGCCTCTCCGTACGCACCCAGAGTACAACAGACCCTTGCTCGCTAACGACCTCATGC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCTGCAGTGCGTGAACGTGTC 487
                                                                                                                                                                                                                                                                      GTGAGCTCACGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATCAAGTIGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-----
                                                                                                                                                                                                                                                                                                                              TCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAGAGCCAGGGAGCCAGATGGTGGAGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTGCTCGGGCG 74
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 777)
1 (bases 1 to 777)
Huang,G.M., Ng,W., Farkas,J., Chen,L., Liang,H.A., Gordon,D.,
Yu,J. and Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leroy Hood
University of Washington
Department of Molecular Biotechnology,
Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostate Cancer Expression Profiling by cDNA Sequencing Analysis Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3138767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Guyang Matthew Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               huanggm@yahoo.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/map="960H11; 6; 6p21.31-6p22.1; 21q"
/map="960H11; 6; 6p21.31-6p22.1; 21q"
/clone_lib="tumor2"
/note="Organ: Prostate; Vector: pBluescript; Directional
/note="Organ: Prostate; Directional
/no
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81.9%;
                                                                                                          ----CAGAATGCTACCGTGCTGCAGTGCGTGAACGTGTC 410
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Pred. No. 9.6e-106;
0; Mismatches 48;
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COMMENT
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AA503963/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (301) 496-1530

Email: Robert_Strausberg@nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo
M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sec
Clone distribution: NCI-GGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 1244 Std Error: 0.00
Seq primer: ~40ml3 fwd. ET from Amersham
High quality sequence stop: 144
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1 (bases 1 to 404)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 144.
Location/Qualifiers
                         64
                /tissue_type="prostate"
/lab_host="DHIOB"
/note="Vector: pAMPIO; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel average insert size 600 bp.

a 91 c 159 g 90 t
                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:954696"
                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Pr5"
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RESULT 3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
AI686689
g4897983
                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 569)

1 (CGAP http://www.nobi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                                                                                                                                                    AI686689 569 bp mRNA EST 27-MAY-1999 tu35g11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253092 similar to TR:Q92046 Q92046 PREPROTRYPSIN PRECURSOR;, mRNA
                                                                                                                                                                         Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein,
                                                                                   Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                        Unpublished (1997)
On Jun 5, 1998 this sequence version replaced g1:3189584
                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                   Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                    AI686689.1 GI:4897983
                                                             primer: -40UP from Gibco
                                   quality sequence stop: 444.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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95.0%;
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Mismatches 19
                                                                                                                                                                           M.D.,
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                                                                                                               Sequencing Center 
information can be
                                                                                                                                                                           Ph.D.,
                                                                                                                                                                                                                                                                               Project (CGAP),
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                                                                                                                                                                              Michael
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Query Match
Best Local Similarity
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                                                                                                                                                                                                      AA551449 415 bp mRNA EST 05-SEP-1997 nj55e05.si NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:996416 similar to SW:KLKA_MOUSE P15946 GLANDULAR KALLIKREIN K11 PRECURSOR
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     AA551449
                                                                                                                         AA551449.1
                                                                                                                                                                                          mRNA sequence.
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with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.

a 150 c 170 g 124 t
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/dev_stage="adult"
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/clone_lib="NCI_CGAP_Pr28"
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83.0%;
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                                                            CAGTAAGCTCTATGACCCGCTGTACCACCCCCAGCATGTTCTGCGCCCGGCGGAGGGCAAGA 568
    CAGAAGGACTCCTGCAACGGTGACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCA 628
                                          CAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGA
                                                                                                                    ----CAGAATGCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGTGTCTGAGGAGGTCTG
                                                                                                                                                                                                                                                                      ACTCTTGCCTCGTTTCTGCCTGGCGCTCTGCTGCCGGCGAACGG-------
                                                                                                                                                                                                                                                                                                                                                   TGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGGGA 328
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                                                                                                                                        AGGCAGAATGCCTACCGTGCTGCAGTGCGTGGAGGTGCTGTGGTGGTGTCTGAGGAGGTCTG 508
                                                                                                                                                                                                                                  TGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGCTGACCCAGAGCTCTGCGTCCC 448
                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chua
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Cone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 640 Std Error: 0.00
Seq primer: ~40ml3 fwd. ET from Amersham
High quality sequence stop: 412.
Location/Qualifiers
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Unpublished (1997)
On May 9, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 415)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:996416"
/clone_lib="NCI_CGAP_Pr9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="normal prostatic epithelial cells"
/lab_host="DH108"
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JOURNAL COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 885 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 256.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: (301) 496-1550

Email: Robert_Strausberg@nh.gov

Tissue Procurement: W. Marston Linehan, M.D., Rod

M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome

Clone distribution: NCI-GCAP clone distribution

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1406821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                           169
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                   /note-"organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:995579"
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                                                                                                                                                                           22.98;
95.78;
                                                                                                                                                      Score 290.2; DB 34; Length Pred. No. 1.3e-60; Mismatches 13; Indels
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               AACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGC
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A1557025 7:
PT2.1_10_F05.r 1
A1557025
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Prostate Cancer Expression Profiling by cDNA Sequencing Analysis Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Washington Department of Molecular E Washington, Seattle, WA STel: 5166280100
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
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/clone_lib="tumor2"
/clone_Togan: Prostate; Vector: pBluescript; Directional
/notee"Organ: Prostate; Vector: pBluescript; Directional
cDNA library was constructed using Lambda ZP II kit
(Stratagene). mRNA was extracted from a frozen prostate
tumor tissue (Mayo Clinics)."
49 others
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/db_xref="taxon:9606"
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tumor2 Homo sapiens cDNA
                                                                                                                                                            Score 241.2; DB 48;
Pred. No. 1.1e-48;
0; Mismatches 26;
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Best Local Similarity 88.8
Matches 231; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Centucle Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 th
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nk52c07.s1
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 258.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                          /tissue_type="low-grade prostatic neoplasia"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
prostate intraepithelial neoplasia (high-grade), cDNA
made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600
                                                                                                                                                                                                                                                                                                                /map="17q21"
/clone="IMAGE:1017132"
                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Pr7"
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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      Score 209.2; DB : Pred. No. 4.2e-41; 0; Mismatches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA552779 229 bp mRNA EST 08-SEP-1997 nk57a10.s1 NCI_CGAP_Pr7 Homo sapiens cDNA clone IMAGE:1017594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
On Jan 25, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 229)
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                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 419
                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                            primer:
                                                                                                                                                                                                                                                                                                             primer: -40ml3 fwd. ET from Amersham
quality sequence stop: 215.
    Location/Qualifiers
49
                                       /note="Organ: prostate; Vector: pAMP10; mRNA made from prostate intraepithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600
                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1017594"
/clone_lib="NCI_CGAP_Pr7"
                                                                                                                                /tissue_type="low-grade prostatic neoplasia"
/lab_host="DH10B"
                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contains MSR1.b3 MSR1 repetitive element ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                    Std Error: 0.00
94
                                          on agarose gel, average insert size 600 bp
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JOURNAL COMMENT
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AUTHORS
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AA603977/c
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                                                                                                                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
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Seg primer: 40ml3 fwd. ET from Amersham
High quality sequence stop: 231.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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no47a09.sl
                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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On Sep 12, 1996 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/sex="male, pooled"
/fissue_type="prostate tumor"
/lab_host="$OLR (Kanamycin resistant)"
/note="Organ: prostate; Vector: Bluescript SK-; Site_1:
EcoRI; Site_2: XhO1; Cloned unidirectionally. Primer:
Oligo dT. Pooled prostate tumors. 5' adaptor sequence:
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1103800"
/clone_lib="NCI_CGAP_Pr23"
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90.4%;
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Pred. No. 7.6e-39;
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ORGANISM
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AI674521/c
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Best Local S
Matches 197
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TITLE
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Unpublished (1997)
On Mar 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI674521 218 bp mRNA EST 19-MAY-1999 wc39g02.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321042 similar to contains MSRI.t2 MSRI repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g4875001
                                                                                                                                                                                                                                            Seq primer: -400p from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
AI674521
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                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mar 16, 1998 this sequence version
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3 7 c 78 g 80 t
/note-"Organ: prostate; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification.
                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                  /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                           /sex="male"
                                                                                                                                           /clone_lib-"NCI_CGAP_Pr28"
                                                                                                                                                                /clone="IMAGE:2321042"
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92.1%;
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Pred. No. 3.8
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158
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                                                                                                                                                                                                    Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Peiligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Well, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGTGCCCCCTTGTGGNANGTTGACCCAACCTTACCAGTTGGTTTTTCATTTTTNGTCCC 1217
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The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
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                                                                            Contact: Kerlavage,
Bioinformatics
                                                                                                                                                            On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA336074.1
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Best Local Similarity
Matches 176; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAGAGCCAGGGGAGCCAGATGG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182
                                                Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188)
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wb97b12.x1 NCI_CGAP_Pr28
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For clone availability.

For clone availability additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI6758:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                      www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anatomy
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primer:
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                                                                                                                                                                                        Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: endometrium; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
65 c 63 g 38 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="ATCC (inhost):138014"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib-"Endometrial tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Homo sapiens"
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  -40UP
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  from Gibco
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Pred. No. 4.3e-33;
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IMAGE:2313599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169;
                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
Unpublished (1997)
On Apr 14, 1993 this sequence version replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           no34h04.s1 NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1102615 3',
                                                                                                    Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
AA595489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA595489
                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution of through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note-"organ: prostate; Vector: pTasmid DNA from the
normalized library NCI_CGAP_PT22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.

a 31 c 61 g 53 t
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/sex="male"
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/clone="IMAGE:2313599"
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92.9%;
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Pred. No. 5.6e-31;
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                    Sequencing Center
information can be
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RESULT 14
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Matches 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:430269
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
                                                                                                                                                                                                                                                                                                                    M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA583052
                                      Insert Length: 667
                                                                                                                               cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                             cDNA Library Preparation: M. Bento Soares, Ph.D.
   primer:
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//db_xref="taxon:9606"
//clone="IMAGE:1102615"
//clone="IMAGE:1102615"
//clone="IMAGE:1102615"
//clone="IMAGE:1102615"
//clone=lib="NCI_CGAP_Pr23"
//sex="male, pooled"
//tissue_type="prostate tumor"
//lab_host="SOLR (kanamycin resistant)"
//lab_host="Primariant of the control of the control
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-40ml3 fwd. ET from Amersham
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Pred. No. 5.1e-28;
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Local Similarity 85.4%;
les 140; Conservative
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1 (bases 1 to 517)

Hillier.L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA293UZ7 517 bp mRNA EST 12-AUG-1997 zt54a12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:726142 5', similar to TR:G940540 G940540 SERINE PROTEASE
High quality sequence stop: 471.
                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                               4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                   Washington University
                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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/clone_lib="NCI_CGAP_Co9"
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/lab_host="DH10B"
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/sex="Female"
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/db_xref="GDB:5938189"
/db_xref="taxon:9606"
/clone="IMAGE:726142"
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Pred. No. 6.3e-17;
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Wang, K.
Direct Submission
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1 (bases 1 to 1347)
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                                    2 (bases 1 to 1347)
Nelson, P.S., Gan, L.,
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Best Local Similarity 87.0
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/db_xref="PID:94512030"

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/map="19q13"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5900)
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QAALVMENELFCSGYLYHPQWYLSAAHCFQNSYTIGLGLHSLEADQEPGSQMYEASLS
YRHPEYNRPLLANDLMLIKLDESYSESDTIRSISIASQCPTAGNSCLYSGWGLLANGR
MPTYLQCYNYSYVSEEYCSKLYDPLYHPSMFCAGGGHDQKDSCNGDSGGPLICNGYLQ
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Homo sapiens kallikrein-like protein 1 KLK-L1 gene,
AF135023.
94589272
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Yousef,G.M., Luo,L.Y. and Diamandis,E.P.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-MAR-1999) Pathology and Laboratory Medicine, I Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4740)

Yousef,G.M., Luo,L.Y. and Diamandis,E.P.

Identification of novel human kallikrein-like genes on chromo:
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LCKFTEWIEKTVQAS"
1275 c 1308 g 1051 t
                                                                                                                                               /translation="SLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVLVHPOW
VLSAAHCFQNSYTIGLGLHSLEADQEPGSQMVEASLSVRHPEYNRPLLANDLMLIKLD
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/db_xref="GI:4589273"
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/product="kallikrein-like protein 1 KLK-L1"
join(<2263. .2425,2847. .3097,3181. .3317,4588.
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/db_xref="taxon:9606"
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            37.5%;
Score 474.8; DB 42;
Pred. No. 9.3e-100;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens kallikrein 4 (KLK4) gene,
AF148532
95020095
                                                                                                                                                                                                                                                                                                Stephenson, S.A., Verity, K., Ashworth, L. and Clements, J.A. Localization of a new prostate specific antigen-related serine protease gene, KLK4, is evidence for an expanded human kallikrein (KLK) gene family cluster on chromosome 19q13.3-13.4
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4385)
                                                                                                                                                                                                                      Submitted (03-MAY-1999) School of Life Science, Queensland University of Technology, George Street, Brisbane, Queensland
                                                                                                                                                                                                                                                             2 (bases 1 to 4385)
Stephenson, S.A., Ashworth, L. and Clements, J.
                                                                                                                                                                                                                                                                                      (KLK) gene
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                                                                        /gene="KLK4"
/product="kallikrein
<551. >4352
                                                                                                               4200.
                                                                                                                       /map="19q13.3-q13.4"
join(<551._.611,1875. .2037,
 /codon_start=1
/product="kallikrein
                         function="serine protease"
                             /gene="KLK4"
                                                            'gene="KLK4"
                                                                                                                                                  /chromosome="19"
                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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2 (bases 1 to 1140)
Simmer, J.P., Fukae, M., Tanabe, T., Yamakoshi, Y., L
Margolis, H.C., Shimizu, M., Hu, C.-C. and Bartlett,
Direct Submission
Submitted (24-OCT-1996) Pediatric Dentistry, Univ
                                                                                                                                         Simmer, J.P., Fukae, M., Tanabe, T., Yamakoshi, Y., Uchida, T., Xue, J., Margolis, H.C., Shimizu, M., Hu, C.-C. and Bartlett, J.D. Purification, Characterization and Cloning of Enamel Matrix Serine
                                                                                                                                                                                                                                                                                                                                                                                                                    SSU76256
Sus scrofa
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetariodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1140)
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Sus scrofa
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/translation="MATAGNPWGWFLGYLILGVAGSLLYSGSCSQIINGEDCSPHSQPW
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VRHPEYNRPLLANDLMLIKLDESVESDTIRSISIASQCFTAGNSCLVSGWGLLANGR
MPTVLQCYNVSUYSEEVCSKLYDPLYHPSMFCAGGGQDQKDSCNGDSGGPLICNGYLQ
GLVSFGKAPCGQVGVPGVYTNLCKFTEWIEKTVQAS"
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                                                                   CGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTTTCCAGAACTCCT 121
                                                                                                                                                                                                                                                                                                                                                                 GCAGCCGGCACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTGCT 61
                       TGGAGGCCAGCCTCTCCGTACGGCACCCAGAGTACAACAGACCCTTGCTCGCTAACGACC 241
                                                                                                                                                                                                           GGGGCGTCCTGGTGCATCCGCAATGGGTGCTGTCAGCCGCACACTGCTTCCAAAATTCCT
                                                                                                                                                                                                                                                                                                                                                 GCAACCCCCACTCGCAGCCCTGGCAGGCGGCACTGTTCCTGGAAGACGACTTTTTCTGCG
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     restereceasteces
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="the preprotein is cleaved following His30 activating the serine proteinase; the active proteinan apparent molecular weight of 34 kDa and a derive molecular weight of 24 kDa"
/product="enamel matrix serine proteinase 1"
order(17. .179,549..551)
/note="disulfide bond"
order(234..236,282..284)
/note="disulfide bond"
/note="disulfide bond"
/note="disulfide bond"
/note="disulfide bond"
/note="disulfide bond"
/note="encodes catalytic triad"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="encodes potential glycosylation location; yields
blank cycle during protein sequencing"
order(408. .410,789. .791)
/note="disulfide bond"
order(510. .512,705. .707)
/note="disulfide bond"
order(675. .677,750. .752)
/note="disulfide bond"
a 366 c 295 g 234 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sus scrofa"
/db_xref="taxon:9823"
69. .140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTAAGNPWGWFLGYLLLGITGSLAFINGGHIINGEDCNPHSOPW GAALFLEDDFFCGGVL/HPGWYLSAAHGFQNSYTIGLGLHNLEDEQDFGSQMMEASLS IQHPEYNEPSMANDLMLIKLKESVSLSDTVRNISVVSQCPTPGDSCLVSGWGRLASGR LPQVLQCVNISVASEEYCKARYGPVYHPSMFCAGGGQDQKDSCHGDSGGPLICNGSLQGLYSFGQAQCGQPNVPGVYTNLCKFTDWIQTTIQAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preprotein is 69. .833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product "enamel matrix serine
/protein_id="AAB94638.1"
/db_xref="piD:92737921"
/db_xref="GI:2737921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="EMSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="the signal peptide is cleaved after
preprotein is secreted into the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete
AF019979
                                                                                                                                                                                                         Submitted (18-AUG-1997) Pediatric Dentistry, University Health Science Center at San Antonio, 7703 Floyd Curl Dr Antonio, TX 78284-7888, USA
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus enamel matrix serine proteinase 1 precursor,
                                                                                                                                                                                                                                                         Simmer, J.
Direct Submission
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Eutheria; Rodentia;
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maturation"
/note="EMSP1"
/codon_start=1
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52. .126
52. .819
                                                                                                   /organism="Mus musculus"
/strain="Swiss-Webster"
/db_xref="taxon:10090"
/cell_type="ameloblast"
                                                                                                                                                                                       Location/Qualifiers
                                                   function-"degradation
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        GCTCCCCACACTCGCAACCCTGGCAGGCGGCACTGTTCTCCAGAAGACGGTTTTTTCTGCT
                                                  AACCGTCCAGGCCAGTTAACTCTGGGGAACTGGGAACCCATGAAATTGACCCCCAAATACA
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                                                                                            GCAGCCTGGCATACCAAGTGTCTACACCAATCTCTGCAAGTTCACTAACTGGATCCAGAC
                                                                                                               CCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAA 721
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WQAALESEDGFFCSGVLVH9QWVLSAAHCLQESYIVGLGCHILKGSQEPGSRMLEAHL
SIQHPNFUNDSFANDLMLIKLMESVIESNTIRSIPATQCPTPGDTCLVSGWGQLMG
KLPSLLQCVNLSVASEETCRLLYDPVYHLSMFCAGGGQDQKDSCNGDSGGPIVCNRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="
145. .8
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127. .144
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/protein_id="AAC98894.1"
/db_xref="pID:g4090847"
/db_xref="GI:4090847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.5%;
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Pred. No. 8.1e-62;
0; Mismatches 296;
                · ACTGACTACAAGGCCCACATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu,S., Attix,C., Andreise,T., Trankheim,M., Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G., Kronmiller,B., Arellano,A., Montgomery,M., OW,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and Carrano,A.V.

Sequence analysis of an -700 kb region in 19q13.4 between D19S268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-OCT-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,
Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J.,
Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 35197)
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                                                                                                                                                                      /note="Cosmid library LL19NC03 was constructed at LLNL from flow-sorted chromosomes from human-hamster hybrid 5HL2-B which carries chromosome 19 as its only human chromosome."
  frame: 251. .
                                                                        /note="BLASTX similarity to Q08509 (311. .346); match: 0.52, score: 3.3e-23; database searched: nr; EPIDERMAL GROWNH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >pir[|S3998] eps8 protein - mouse >g1|309217 (L21671) Eps8 [Mus"
                                                            eps8 protein -
155. .243
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="R31855"
/note="predicted exon, program: grail
frame: 0, quality: excellent, score:
251. .279
                                                                                                                                                        148. .255
                                                                                                                                                                                                                                                      library
                                                                                                                                                                                                                                                                                          /map="19q13.4 between D19S268 and /cell_line="5HL2-B"
                                                                                                                                                                                                                                                                                                                                /chromosome="19"
                                                                                                                                                                                                                                                                        /clone_lib="LL19NC03 R chromosome 19-
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                    program: grail2exons_human_1.3
ellent, score: 98.000"
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frame: 1, quality: excellent, score: 75.000-DDS
similarity to overlapping ESTs:-R34158 yh83h09.s1 Homo
sapiens cDNA clone 156385 3' similar to SP:33983 S39983
EPS8 PROTEIN; (56. 194); 94% identity.--R80263 y196h06.s1
Homo sapiens cDNA clone 147131 3', (46. 186); 94%
identity.--H13945 y108d11.s1 Homo sapiens cDNA clone
148149 3' similar to SP:S39983 S3983 EPS8 PROTEIN;
(21. 161); 94% identity."
n complement(1621. 1652)
/rpt_family="GC_rich"
1679. 1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MIR"
3607.3702
/rpt_family="MIR"
3904.4036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="BLASTX similarity to Q08509 (343. .373); match: 0.51, score: 3.3e-23; database searched: nr; EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 pir||S39983 eps8 protein - mouse >g1|309217 (L21671) Eps8 [Mus" 338. .412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MSR1" 3160. .3240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eps8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note**DDS similarity to overlapping ESTs:-R34158 //note**DDS similarity to overlapping ESTs:-R34158 syh83h09.sl Homo sapiens cDNA clone 136385 3' similar to Sp:S39983 ESPS8 PROTEIN; (195. .223); 97% identity.--R80263 y196h06.sl Homo sapiens cDNA clone 147131 3'; (187. .215); 97% identity.--H13945 yj08d11.sl Homo sapiens cDNA clone 148149 3' similar to SP:S39983 ESPS8 PROTEIN; (162. .190); 93% identity."
                                    /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 90.000-DDS similarity to: '(4124. 4215) R34158 yh83h09.sl Homo sapiens cDNA clone 136385 3' similar to SP:S39983 S39983 EPS8 PROTEIN; (272. 364); 94% identity.--(4124. 4136) H13945 y)08d11.sl Homo sapiens cDNA clone 148149 3' similar to SP:S39983 S39983 EPS8 PROTEIN; (324. 336); 10
                                                                                                                                                                                                                                                             PROTEIN; (191. 323); 95% identity."
3989. 4036
'note="DDS similarity to R34158 y83h09.sl Homo sapiens cDNA clone 136385 3' similar to SP:S39983 S39983 EPS8 PROTEIN; (2244. 271); 100% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 99.000-DDS similarity to overlapping ESTS:-(3904. 3988) R80263 y196h06.sl Homo sapiens cDNA clone 147131 3'; (216. .300); 96% identity.--(3904. .4036) H13945 y108011.sl Homo sapiens cDNA clone 148149 3' similar to SP:S39983 S39983 EPS8 PROTEIN: (191. .323); 95% identity."
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frame: 1, quality: excellent, score: 100.000"
517. .660
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                                          .336); 100%
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/note="BLASTN similarity to D25793 (1..132); match: 0.9 score: 2.8e-45; database searched: est; Human colon 3'directed MboI cDNA, HUMGSO4161, clone cm1029."
n complement(6867..6897)
/rpt_family="GC_rich"
1 7429..8057
                                                                                                                                                                                                                                                                                                                                                                                                               complement(9535. 9621)

/note="predicted exon, program: grail2exons_human_1.3,
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 92.000"

complement(9677. 9763)

/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score: 100.000"

complement(10285. 10389)

/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000"

complement(10580. 10551)

/rpt_family="GC_rich"

complement(10685. 1.0725)

/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 85.000"

complement(10810. 10931)

/reme: 1, quality: excellent, score: 85.000"
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/rpt_family="AluSx"

8979. .9294

/note="DDS similarity to T23821 seq1081 Homo sapiens cDNA clone b4HB3MA-Cot51.5-HAP-Ft-23 3'; Score: 597 Identity: 311/319 (97%).--Additional EST matches: AI125316, T33476 and many others"

complement(9535. .9621)
complement(11079. .11139)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 83.000--DDS
similarity to R35625 yg66g06.r1 Homo sapiens cDNA clone
38310 5', (254. .318); 91% identity."
complement(11216. .11296)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score: 100.000--DDS
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/note="DDS similarity to R34157 yh83h09.r1 Homo sapiens CDNA clone 136385 5'. Score: 513 Identity: 268/270 (99%)."
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complement(4817. .4878)
/rpt_family="GC_rich"
                                                                                                                                                                                                                                                             /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 79.000--(10928. 10906) DDS similarity to R35625 yg66g06.rl Homo sapiens CDNA clone 38310 5'; (319. .341); 78% identity."
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frame: 2, quality: excellent, score: 95.000"
4777. .4951
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/note="predicted exon,
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ellent, score: 93.000"
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Submitted (22-DEC-1998) Barton P.J.R., Cardiothoracic Surgery, National Heart & Lung Institute, Imperial College of Science, Tech. & Med., Dovehouse Street, London SW3 6LY, UK On*Dec 29, 1998 this sequence version replaced gi:1524065.
                                                                                                                                                                       Direct Submission
Submitted (15-AUG-1995) P.K. Bhavsar, Cardiothoracic Surgery,
National Heart & Lung Institute, Imperial College of Science, Tech. &
Med., Dovehouse Street, London SW3 6LY, UK
                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 6592)
Barton, P.J., Cullen, M.E., Townsend, P.J., Brand, N.J., Mullen, A.J., Norman, D.A.M., Bhavsar, P.K. and Yacoub, M.H.
Norman, D.A.M., Bhavsar, P.K. and Yacoub, M.H.
Close physical linkage of human troponin genes: organization, sequence, and expression of the locus encoding cardiac troponin I and slow skeletal troponin T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6592)

Bhavsar, P.K., Brand, N.J., Yacoub, M.H. and Barton, P.J.R.
Isolation and characterization of the human cardiac troponin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSCTPIIT5 6592 bp
Homo sapiens TNNI3 go
X90780 X90781 X90782
                                                                                            Barton, P.J.R.
Direct Submission
                                                                                                                                Revised by [3]
4 (bases 1 to 6592)
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.7e-38;
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                Similarity
                                                                                             1424
   Conservative
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                                                                                        /gene="TNNI3"
6568. .6573
/gene="TNNI3"
/note="putative"
a 1836 c 2048
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                                                                                                                                                                                                                               4633. .4809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="madgssdaareprpapapirrrssnyrayatephakkkskisas
RKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQLHA
RVDKVDEERYDIEAKVTKNITEIADLTQKIFDLRGKFKRPTLRRVRISADAMMQALLG
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/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="cardiac troponin
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/db_xref="PID:e196058"
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2507. .2638,4009. .4098,4633. .4809,6442. .6525)
/gene="TNNI3"
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join(1107. .1260,1532. .1544,1706. .1789,2195. .:

2507. _2638,4009. .4098,4633. .4809,6442. .6592)
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/gene="TNNI3"
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/gene="TNNI3"
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                15.1%;
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                             Length 6592;
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Gaps

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/percial /gene="xrcC1" /note="exon 3; G00-120-737" 2492225080 /partial /gene="xrcC1"	exon 4/24. 4816 /gene="xxCC1" /note="exon 2; G00-120-737" exon 18706. 18816		/gene="XRCC1" exon 42684318	/tissue_lib="LL19NCO2-F2" /map="19q13.2" gene 426836195	/db_xfet="tdxOn:9900" /cell_tipe="tymphocyte" /dev_stage="adult" /tissue_type="blood"	Ce	Stilwagen, S.A., Scheidecker, L. and Tebbs, R.S. Genomic sequence comparison of the human and gene regions Genomics (1995) In press	Euk Eut	SION WORDS RCE	LOCUS HUMXRCC1G 37785 bp DNA DEFINITION Human XRCC1 DNA repair gene, genomic. ACCESSION L34079 NTO G643716	RESULT 9	Qy 1136 CCACCTAGATTTTCCCT 1152	Oy 1076 TTCCCCAGACCCAGAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAATG 1135	Qy 1016 GGGTTGAGGCCCCCAACCCCTCCTTCAGAGTCAGAGGTCCAAGGCCCCAACCCCTCG 1075	Qy 956 GCCCTCCTCCATCAGACCCAGGAGTCCAGACCCCCAGCCCCTCCCT	Qy 903 AGACCCAGGAGTCCAGACCCCCAGCCCTCCTCCAGACCCAGGAGTCCA 955	Qy 843 CAGGCCCCAGCCCCTCCTCCAAACCAAAGGTACAAGATCCCCAGCCCCTCCTCCTC 902	Qy 783 CCTGCGGAAGGAATTCAGGAATATCTGTTCCCAGCCCTCCTCCCTC
Query Match 15.0%; Score 190.2; DB 9; Length 37785; Best Local Similarity 74.6%; Pred. No. 2.4e-34; Matches 302; Conservative 0; Mismatches 91; Indels 12; Gaps 5;	/gene="XRCC1" /gene="XRCC1" /note="exon 17; G00-120-737" BASE COUNT 8717 a 9329 c 9806 g 9929 t 4 others ORIGIN	/note="exon 16; G00-120-737" exon 36082. 36195 /partial	/partial	/gene="XRCC1" /gene="XRCC1" /note="exon 15; G00-120-737" exon 3589935975	/partial	/gene="XRCC1" /note="exon 13; G00-120-737" exon 33629: .33768	/gene="XRCC1" /gene="XRCC1" /note="human chromosome 19-specific tandem repeat, pE670" /note="human chromosome 19-specific tandem repeat, pE670" /notrial	/gene="XRCC1" /gene="XRCC1" /note="exon 12; G00-120-737" satellite complement(3300133360) /partial	/partial /gene="XRCC1" /note="exon 11; G00-120-737" 32859. 32991 (nartial	/partial /gene="XRCC1" /note="exon 10; G00-120-737" exon 32609 32702	/gene="XRCC1" /note="exon 9; G00-120-737" exon 28039 .28155	/gene="AKCC1" /note="human chromosome 19-specific tandem repeat, pE670" exon 2745127709 /partial	/gene="XRCC1" /gene="xRCC1" /note="exon 8; 600-120-737" satellite complement(2700827410) /partial /partial	/9ene= ARCCI /note="exon 7; G00-120-737" exon 2681826929 /partial	yene ARCCI / Yene ARCCI / Young Thuman chromosome 19-specific tandem repeat, pE670 exon 2663526744 /partial / Partial / Par	yene ARCL1 /note="exon 6; G00-120-737" satellite complement(2634226484) /partial /con_myscol"	/gene="XRCC1" /note="exon 5; G00-120-737" exon 2621426325 partial /Gene_"XRCC1"	/note="exon 4; G00-120-737" exon 2604326117 /partial

chromosome

Mammalia;

novel

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KEYWORDS
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                                                                                                                                                               ATTCAGGAATATCTGTTCCCAGCCCCTCCCTCCCTCAGGCCCAGGAGTCCAGGCCCCAGC 854
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                        CNTCAGACCCAGGAGTCCAGACCCCCAGCCCCTCCTCCTCAGACCCAGGGGGTTGAGGC 1025
                                                                          TCCAGACCCCCAGCCCCTCCTCCTCAGACCCAGGAGTCCAG------CCCCTCCTC
                                                                                                                                                  ACTTAGGAGTCCAGGCTCCCGGCCCCTCCTTCCTCAGACCCAGGAGTCCAAGCCCCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
I34189
                                                                                                                                                                                                                                                                                                     Patent: US 5595900-A 5 21-JAN-1997;
Location/Qualifiers
1.8174
                                                                                                                                                                                                                                                                                                                                                   Methods and products for the synthesis of oligosaccharide structures on glycoproteins, glycolipids, or as free molecules, for the isolation of cloned genetic sequences that determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g1824980
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/organism="unknown"
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Pred. No. 5.1e-33;
0; Mismatches 64;
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Best Local Similarity
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                      AGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGACCCAGAGGTNNAG-GTCCCAGC
                                                                                                 CCAGGAGTCCAGAGCCCCAGCCCTCCTCCCTCAGACACAGAAGGCCTA
                                                CCCCCAGCCCTCCTCAGACTCATGAGTCCAGACCCCCAGCCCCTCCTCCTCAG
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87165892
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Chromosome 19, long arm
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1 (bases 1 to 281)
Das, H.K., Jackson, C.L., Miller, D.A., Leff, T. and Breslow, The human apolipoprotein C-II gene sequence contains a no chromosome 19-specific minisatellite in its third intron
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Human 37 b
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K03500.1 GI:337672
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ilarity 82.4%;
Conservative
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263. 281
/note="sat rpt partial
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226...2
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/db_xref="taxon:9606"
/clone_lib="COS 4C"
/cell_line="JY"
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Pred. No. 1.5e-30;
0; Mismatches 38
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855 CCCTCCTCCAAACCAAGG-GTACAGATCCCCAGCCCCTCCTCCTCCAGACCCAGGAG
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                                             ATTCAGGAATATCTGTTCCCAGCCCCTCCTCCCTCAGGCCCCAGGAGTCCAGGCCCCCAGC 854
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Structure and expression of H-type GDP-L-fucose:beta-D-galactoside
2-alpha-L-fucosyltransferase gene (FUT1). Two transcription start
sites and alternative splicing generate several forms of FUT1 mRNA
J. Biol. Chem. 272 (11), 7501-7505 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimura, Kurume University, School of Medicine, Department o Medicine; 67 Asahimachi, Kurume, Fukuoka 830, Japan (E-mail)hkimura@kurume.ktarn.or.jp, Tel:0942-31-7554, Fax:0942-31-7700)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larsen,R.D., Ernst,L.K., Nair,R.P. and Lowe,J.B.
Molecular cloning, sequence, and expression of a human
Molecular cloning, sequence, and expression of a human
GDP-L-fucosyltransferase
that can form the H blood group antigen
Proc. Natl. Acad. Sci. U.S.A. 87 (17), 6674-6678 (1990)
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Homo sapiens peripheral leukocytes DNA
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                                                                                                                                                                                                                                                            /gene-"FUT1"
                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19q 13.3"
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1. .1665
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Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J.,
Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J.,
Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G.,
Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G.,
Kronmiller, B., Arellano, A., Montgomery, M., Ow, D., Nolan, M.,
Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V.
Sequence analysis of a 2.5 Mb region in 19913.2 containing a
                                                                                                                                                                                                                                                                                                                           Submitted (06-AUG-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from g centromere to telomere. BAC 338531 (CIT-HSP 490g23) is adjacent to cosmid F24498 to the left and overlaps BAC 52850 (CIT-HSP 6117) to the right by approximately 35 kb. Accession does not represent the sequence of the entire BAC clone insert at this time. Additional chr 19 map and sequence
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1154. .1359
                                                                                                                                                                     /organism="Homo sapiens"
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/clone="490g23"
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                                                                                                         /map="19q13.2 between BCKDHA and /clone_lib="CIT-HSP"
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oares senescent fibroblasts NbHSI 323296 3' similar to gb:M20882 BETA-1 GLYCOPROTEIN E PRECURSOR ; 99% identity(1649416238) enescent fibroblasts NbHSF Homo s ' similar to gb:M23575			complement(14138/rpt_family="AluSg" complement(14308	<pre>/rpt_family="MER11A complement(13622. /rpt_family="HERVK"</pre>	comp /rpt		/rpt_ 1269;	/rpt 1239	n complement(1208112261) /rpt_family="MIR" - 13867 13867	1117: /rpt			79378213		747	/rpt_ramily="Alux complement(7329.	-	comp	/rpt_family="Alu" complement(5095.	/rpt_		4129 7129	n 3807		/rpt_family="Alusx" 33993495	/rpt 2634	/rpt_fa	/rpt
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<pre>complement(2415824188) /note="BLASTN similarity to T39410 (4777); match: 0.96, score: 7.0e-47; database searched: est; ya05f02.r3 Homo sapiens cDNA clone 60603 5' contains Alu repetitive element" complement(2415824188)</pre>	/note="BLASIN SIMILATILY TO 14994 (120); match: 0.98, score: 1.9e-92; database searched: est; ya76h05.rl Homo sapiens cDNA clone 67641 5' similar to gb:M20881 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN D PRECURSOR"	gb:M20881 ECURSOR"	<pre>complement(2370423760) /note="BLASTN similarity to T49544 (203259); match: 0.96, score: 1.9e-92; database searched: est; ya76h05.r1</pre>	<pre>score: 7.0e-47; database searched: est; ya05f02.r3 Homo sapiens cDNA clone 60603 5' contains Alu repetitive element,."</pre>	PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR -" complement(2368523760) /note="BLASTN similarity to T39410 (75150); match: 1,	/note="BLASTN similarity to T39371 (75274); match: 1, score: 1.7e-95; database searched: est; ya05b01.rl Homo	beta-1-glycoprotein 11 form r precursor - human" complement(2356123760)	<pre>complement(250/23/38) /note="BLASTX similarity to (331414); match: 0.86, score: 5.7e-104; database searched: nr; pregnancy-specific</pre>	5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN); (1183); 99% identity."	John John John John John John John John	beta-1-glycoprotein 11 form w precursor - human" complement/33806	Complement(2320423738) /note="BLASTX similarity to (331495); match: 0.89, score. 3 0o-158 . Astabase searched: nr: programmer.spooffic	rpt_family="L1MB5" /rpt_family="L1MB5"	. 2029920483 		1967919978 /rpt_family="L1"		<pre>complement(19312. /rpt_family="MIR"</pre>		5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPPOTEIN C PRECURSOR (HUMAN); (184267); 100%	complement(183461842) /note="DDS similarity to W49630 zc42h12.rl Soares senescent fibroblasts NDHSF Homo sapiens cDNA clone 325031	GLYCOPROTEIN E PRECURSOR (HUMAN); (441402); 100%	senescent fibroblasts NbHSF Homo sapiens cDNA clone 323296 3' similar to gb.M20882 PREGNANCY-SPECIFIC BETA-1		17252174 /rpt_family		(HOMAN); (200324); 99% complement(1666716961) /rot family="aliv"	

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201638 CAGGAGTCCAGGCCCCCAGTCCCTCCTCCCTCAGACCCAGGAGTCCAG-GCCCCAGTGC
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Submitted (22-DEC-1998) Barton P.J.R., Cardiothoracic Surgery, National Heart & Lung Institute, Imperial College of Science, Tech., Med., Dovehouse Street, London Edy, UK On Dec 29, 1998 this sequence version replaced gi:1524065. This sequence is directly followed by the slow skeletal troponin T gene (AC AJ011712, AJ011713)
                                                                                                                                                                                                Submitted (15-AUG-1995) P.K. Bhavsar, Cardiothoracic Surgery, National Heart & Lung Institute, Imperial College of Science, Tech. & Med., Dovehouse Street, London SW3 6LY, UK
                                                                                                                                                                                                                                                                                                                                        Barton, P.J.R., Cullen, M.E., Townsend, P.J., Brand, N.J., Mullen Norman, D.A.M., Bhavsar, P.K. and Yacoub, M.H. Close physical linkage of human troponin genes: organization, sequence, and expression of the locus encoding cardiac tropon and slow skeletal troponin T
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Bhavsar, P.K., Brand, N.J., Yacoub, M.H. and Barton, P.J
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x90780 x90781 x90782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"BLASTN similarity to T39371 (47. .77); match: 0.9 score: 1.7e-95; database searched: est; ya05b01.r1 Homo sapiens cDNA clone 60553 5' similar to SP:A33514 A33514 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR -" complement(24162. .24437)
/note-"BLASTX similarity to (238. .329); match: 0.9,
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/gene="TNNI3"
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6568. .6573
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1075. .1081
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2507. .2638,4009. .4098,4633. .4809,6442. .6525)
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/gene="TNNI3"
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join(1107. .1260
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                                                         Score 165.4; DB 10
Pred. No. 1.3e-28;
0; Mismatches 97;
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REFERENCE AUTHORS TITLE

Barton, P.J.R. Direct Submission

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COMMENT

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Direct Submission Bhavsar, P.K. Unpublished JOURNAL MEDLINE REFERENCE

TITLE

AUTHORS

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TNNI3

SOURCE ORGANISM

Homo sapiens

KEYWORDS

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ACCESSION DEFINITION

RESULT 14
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AB006136.1 GI:3242453
FUT1; alpha (1, 2) fucosyltransferase.
Homo sapiens peripheral leukocytes DNA.
Homo sapiens
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                                                                                                                                                                                                                                              Unpublished (1998)
On Jun 20, 1998 this sequence version Sequence updated (16-Jun-1998).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (04-AUG-1997) to the DDBJ/EMBL/GenBank databases. Yoshiro Koda, Kurume University, School of Medicine, Department of Forensic Medicine: Asahimachi 67, Kurume, Fukuoka 830, Japan (E-mail:ykoda@med.kurume-u.ac.jp, Tel:0942-31-7554,
                                                                                                                                                                                                                                                                                                                 Koda, Y., Soejima, M. and Kimura, H.
Changing transcription start sites in H type
a(1.2)fucosyltransferase gene (FUT1) during differentiation
human Eerythroid lineage
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1 (bases 1 to 4033)
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511. .>578
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hes 236; Conservative
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Pred. No. 3.2e-28;
0; Mismatches 33
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Score 1254; DB 1; 1 Pred. No. 3.9e-296; 0; Mismatches 0;

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Sequence:

PF 25-FEB-1998; U03690.
PR 25-FEB-1998; US-904809.
PR 25-FEB-1997; US-904809.
PR 25-FEB-1997; US-904809.
PR 101-AUG-1997; US-904809.
PR 01-AUG-1997; US-904809.
PR 01-AUG-1997; US-904809.
PR 01-AUG-1997; US-904809.
PR 01-AUG-1997; US-904809.
PR 1011Lon DC, Xu J;
IDR WPI; 98-480805/41.
PI 1011Lon DC, Xu J;
IDR WPI; 98-480805/41.
PT Novel human prostate specific tumour protein and fragments - useful PT for detecting and treating prostate cancers
PS Claim 1; Page 113-114; 141pp; English.
CC This sequence represents a human prostate tumour specific gene, and can CC be used in the method of the invention. The method is for detecting CC prostate cancer comprises contacting a biological sample with an agent CC encoded by this sequence). An antibody which binds to an immunogenic CC contion of the prostate protein, and the method can be used to detect.
CC monitor progression of, or treat prostate cancers. The antibody may calso be conjugated to a therapeutic agent for use in therapy of prostate Homo sapiens. W09837418-A2. V58645 standard; 08-DEC-1998 tumour (first entry) вр; specific gene clone DE2.
specific gene; human; prostate cancer; detection; 1265 256 A; ALIGNMENTS 432 C; 321 ဂ္ 245

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V61250
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V61250 standard; cDNA; 1:
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cDNA sequence of prostate
Prostate; cancer; tumour;
Homo sapiens.
W09837093-A2.
27-AUG-1998.
27-AUG-1998; U3492.
09-FEB-1998; US-020956.
25-FEB-1998; US-806099.
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Best Local Similarity 100
Matches 1265; Conservative
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The present sequence is a new DNA which encodes an immunogenic p of a prostate tumour protein. The encoded immunogen, or the DNA can be used as a vaccine for the treatment of prostate cancer. T was identified by analysis of a subtracted cDNA library obtained subtracting a prostate tumour cDNA expression library with a nor tissue cDNA library.

Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T;
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D111on DC, Xu J;
WPI; 98-609886/51.
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01-AUG-1997; US-9048
(CORI-) CORIXA CORP
Dillon DC, Xu J;
WPI; 98-480805/41.
P-PSDB; W69387.
                 Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers Claim 1; Page 112; 141pp; English.

This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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                                                                                                                                                                                                                                                                                                                                                         Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 104; 130pp; Engilish.

The present sequence is a new DNA which encodes an immunogenic port of a prostate tumour protein. The encoded immunogen, or the DNA its can be used as a vaccine for the treatment of prostate cancer. The was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.

Sequence 1248 BP; 288 A; 424 C; 303 G; 228 T;
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27-AUG-1998: U03690.
25-FEB-1998: US-904809.
25-FEB-1997: US-806596.
01-AUG-1997: US-904809.
(CORI-) CORIXA CORP.
D1110n DC, Xu J;
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08-DEC-1998 (fir
Prostate tumour s
Prostate tumour s
therapy; ss.
Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers

Claim 1; Page 115; 141pp; English.

This sequence represents a human prostate tumour specific gene, and car be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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CDS
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P-PSDB; W69388.
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cDNA sequence of prostate tumour clone prostate; cancer; tumour; vaccine; imm Homo sapiens.

wo9837093-A2.
27-AUG-1998.
25-FEB-1998; US-020956.
25-FEB-1998; US-020956.
25-FEB-1997; US-806099.
01-AUG-1997; US-904804.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI; 98-609886/51.
P-PSDB; W71782.
P-PSDB; W71782.
P-PSDB; W7182.
P-PSDB; W7182.
Claim 3; Page 107; 130pp; English.
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1167 BP; 242 A; 400 C; 287 G; 222 T;
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91.0%;
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No. 3.5e-243;
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                                            Claim 10; Fig 1; 120pp; English.

The sequence is that of the Tub Interactor gene hTI-1 which codes for a putative serine protease. TI genes function in blochemical pathways involved in weight control and related disorders. The products can be used for treating weight disorders, e.g. obesity, cachexia or anorexia nervosa, or a related disorder such as diabetes. The products can also be used to modulate cell cycle progression and apoptosis. They can be used for treating neurodegenerative diseases which are characterised by apoptosis, including Alzheimer's disease, Parkinson's disease, Huntington's choree, amylotrophic lateral sclerosis or spinocerebellar degenerations. The products can also be used for detection, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9812302-A1.
26-MAR-1998.
05-SEP-1997; U15627.
21-JUL-1997; US-897340.
17-SEP-1996; US-715032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens Tub Interactor (hTI-1) gene. serine protease; tub interactor; treatment; obesity; cachexia; serine protease; tub interactor; treatment; obesity; cachexia; anorexia nervosa; diabetes; cell cycle progression; apoptosis; neurodegenerative disease; Alzhelmer's disease; drug screening; Parkinson's disease; Huntington's chorea; detection; diagnosis; amplotrophic lateral sclerosis; spinocerebellar degeneration; si
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drug screening.
Sequence 1386
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V11855;
11-SEP-1998 (fi
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/product= hTI-1 protein
/note= "putative serine
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anorexia nervosa

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Query Match
Best Local Similarity
Matches 1147; Conser

Conservative

81

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Score 871.6; DB 1; Pred. No. 3.8e-203; 3; Mismatches 25;

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CCGCACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTGCTCGGGC 66

Query Match
Best Local Similarity
Matches 737; Conserv

50.7%; 89.0%;

Score 641; Pred. No. 3.9e.

DB 1; 1 .9e-147;

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14-MAY-1998.
31-OCT-1997; U20051.
05-NOV-1996; US-744026.
(INCY-) INCYTE PHARM INC.
Bandman O, Goli SK;
WPI; 98-286933/25.
                                                                                                                                                                                                                                                                                                                                                                 Human prostate-specific kallikrein (HPSK) encoding Prostate-specific kallikrein; HPSK; prostate carcin benign prostate hyperplasia; diagnosis; drug screen: Homo sapiens.

Key

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             V37495 stand
V37495;
07-SEP-1998
Claim 5; Fig 1A-C; 68pp; English.

Claim 5; Fig 1A-C; 68pp; English.

This DNA encodes a human prostate-specific kallikrein (HPSK). A host containing an expression vector comprising the HPSK nucleic acid seque can be used to produce the protein recombinantly. The HPSK products can be used for the diagnosis of conditions or diseases associated with expression of HPSK such as prostate carcinoma and benign prostate hyperplasia. Agonists and antagonists which specifically bind to HPSK modulate its activity can be used for the preparation of treatment of such conditions or diseases. The products can also be used for detection drug screening, especially for the detection of prostate-specific kallikrein (PSK).

Sequence 871 BP; 166 A; 260 C; 258 G; 184 T;
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                                                                                                                                       hyperplasia
Claim 5; Fi
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/transl_except= (pos:412. .414,
/transl_except= (pos:424. .426,
/product= "HPSK protein"
/note= "Xaa = unknown"
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                              WO9837418-A2.
27-AUG-1998.
25-FEB-1998. US-904809.
25-FEB-1997. US-806596.
01-AUG-1997. US-904809.
     (CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI; 98-480805/41.
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                                                                                                                                standard;
prostate specific
                                                                                                                                CDNA;
                                                                                              gene clone DE6.
gene; human; prostate
                                                                                                                                 ВP
tumour
                                                                                                       clone DE6.
protein
and
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fragments
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Best Local S
Matches 477
       Prostate; cancer; tum
Homo sapiens.
W09837093 A23.
27-AUG-1998.
25-FEB-1998; US-02095
25-FEB-1997; US-80609
01-AUG-1997; US-90480
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI; 98-609886/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for detecting and treating prostate cancers

Claim 1; Page 114; 141pp; English.

This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostat
                                                                                                                                         V61251;
V61251;
                                                                                                                     cDNA sequence
                                                                                                                               06-JAN-1999 (first entry)
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477; Conserv
                                                                                                                                                   standard;
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                                      ; U03492.
; US-020956.
; US-806099.
; US-904804.
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comprising
                                                                                                           of prostate cer; tumour;
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 immunogenic
                                                                                                           tumour clone P703 splice variant vaccine; immunogen; clone; ss.
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WO9837418-A2.
27-AUG-1998.
25-FEB-1998; U3-904809.
09-FEB-1997; US-806596.
01-AUG-1997; US-904809.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI; 98-480805/41.
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The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.

Sequence 1459 BP; 427 A; 328 C; 406 G; 295 T;
                                                                                                                                                                                                                                                                                                            08-DEC-1998 (first entry)
Prostate tumour specific gene; human; pro
Prostate tumour specific gene; human; pro
therapy; ss.
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V58648;
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DE CDNA sequence of prostate tumour clone P703 splice variant DE14.

KW Prostate; cancer; tumour; vaccine; immunogen; clone; ss.

S Homo sapiens.

PN W09837093-A2.

PN W09837093-A2.

PP 25-FEB-1998; U3-020956.

PR 25-FEB-1997; US-806099.

PR 25-FEB-1997; US-806099.

PR 25-FEB-1997; US-904804.

PR 25-FEB-1998; US-020956.

PR 25-FEB-1998;
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Claim 1; Page 116-117; 141pp; English.
This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostat
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New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue claim 1; Page 205; 824pp; English.

X41094 to X41347 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in X12261 to X12514, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, chemotactic/
                                                                                                                                                                                                                                                                                      Human secreted protein; EST SEQ ID NO:58
Human; secreted protein; EST; expressed sequence tag; diagnosis;
forensic; gene therapy; chromosome mapping; signal peptide;
upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopoiesis regulation; tissue growth regulation;
reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
thrombolytic; anti-inflammatory; tumour inhibition; ds.
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Duclert A, Dumas Milne
WPI; 99-153778/13.
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X41114;
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01-AUG-1997; US-905135.
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Best Local S
Matches 370
  Isolation of gene conveying post-translational charace.g. the presence of soluble or membrane bound oligo polysaccharide or glycosyltransferase.

Disclosure; Fig 3; 155pp; English.

The DNA encodes a protein sequence capable of functio GDP-Fuc:[beta-D-Gal alpha(1,2)-fucosyltransferase.coded by nucleotides 4782 - 5780 represents the funct The enzyme produced by the DNA sequence can be used i
                                                                                                                                                                                                                                                                                             22-AUG-1991;
14-FEB-1991;
14-FEB-1990;
14-FEB-1990;
14-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokinetic activity, haemostatic and thrombolytic activity, receptor/
ligand activity, anti-inflammatory activity, tumour inhibition activity
or other activities. The products can be used in forensic, gene therapy
and chromosome mapping procedures. The sequences can also be used for
obtaining corresponding promoter sequences. The nucleic acids encoding
the signal peptide can be used for directing extracellular secretion of
a polypeptide or the insertion of a polypeptide into a membrane, or
importing a polypeptide into a cell.
sequence 402 BP; 80 A; 125 C; 121 G; 75 T;
                                                                                                                                                                                                   P-PSDB; R13751.
                                                                                                                                                                                                                         Lowe JB; . WPI; 91-267151/36.
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GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase
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al Similarity 96.4%;
370; Conservative
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; US-480133.
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Pred. No. 1.1e-75;
0; Mismatches 2;
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RESULT 15

Q35908/c
Q35908 standard; DNA; 8174 BF
AC Q35908 standard; DNA; 8174 BF
AC Q35908 standard; DNA; 8174 BF
AC Q35908; G1ycosyltransferase; fucosylt
KW Glycosyltransferase; fucosylt
KW surface; oligosaccharide; ss.
OS Homo sapiens. Location/Qual
FT cds /*tag= a
PN W9402616-A.
PD Q3-FEB-1994.
PD Q3-FEB-1994; U6703.
PR Q0-JUL-1993; U06703.
PR Q0-JUL-1993; U06703.
PR Q0-JUL-1993; US-914281.
PR (UNMI ) UNIV MICHIGAN.
PR Q0-JUL-1993; US-914281.
PR (UNMI ) UNIV MICHIGAN.
PR Q0-JUL-1993; US-914281.
PR A (UNMI ) UNIV MICHIGAN.
PR D1 A fragment encoding a glyce
PT vitro reactions to modify ce
PT vitro reactions to modify ce
PT blood gp. determinants, to p
PS D1sclosure; F1g 3; 249pp; En
CC The sequence 1s that encodin
CC The sequence 1s that encodin
CC Loss of enzyme activity. It
CC modify cell surface oligosac
See also Q56905-12.
S0 Sequence 8174 BP; 1628
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Best Local S
Matches 272
                                                            Query Match 14.6%;
Best Local Similarity 78.2%;
Matches 272; Conservative
                                                                                                                                                              wor JB;
word JB;
word JB;
p-pSDB; R45936.
p-pSDB; R45936.
p-pSDB; R45936.

DNA fragment encoding a glycosyltransferase - can be used for in vitro reactions to modify cell surface oligosaccharide(s) e.g. blood gp. determinants, to protect against transplant rejection bisclosure; Fig 3; 249pp; English.
The sequence is that encoding human glycosyl transferase. The enzyme produced by the DNA may be non glycosylated. This prevents premature loss of enzyme activity. It can also be used in in vitro reactions to modify cell surface oligosaccharide mols. e.g. blood group determinants see also Q55905-11.

Sequence 8174 BP; 1628 A; 2228 C; 2322 G; 1996 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a glycosyltransferase. Glycosyltransferase; fucosyltransferase; surface; oligosaccharide; ss.
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Sequence 8174 BP; 1628 A; 2229 C; 2322 G; 1995 7
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795 ATTCAGGAATATCTGTTCCCAGCCCCTCCTCCTCAGGCCCAGGAGTCCAGGCCCCCAGC 854
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                                                            Score 184.6; DB 1;
Pred. No. 6.7e-36;
0; Mismatches 64;
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Pred. No. 6.7e-36;
D; Mismatches 64;
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          CCAGAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAA 1133
                                                                                  CCCTCCTCCCTCAAACCAAGG-GTACAGATCCCCAGGCCCTCCTCCCTCAGACCCAGGAG
                                                             CCCCAACCCCTCCTTCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGAC
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Search completed: September 25, 1999, 09:56:30 Job time: 8041 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/1na/5B_COMB.seq:*
/cgn2_6/ptodata/2/1na/5C_COMB.seq:*
/cgn2_6/ptodata/2/1na/5D_COMB.seq:*
/cgn2_6/ptodata/2/1na/PCTUS9_COMB.seq:*
/cgn2_6/ptodata/2/1na/backfiles1.seq:*
US-08-744-026-2
US-07-914-281-5
US-08-393-246-5
US-08-393-246-5
US-08-361-395-2
US-08-361-395-2
PCT-US96-04294-1
PCT-US96-04294-1
PCT-US96-04294-3
US-08-557-146-1
US-08-684-862-1
US-08-684-698-3
US-08-6850-129-1
US-08-650-129-3
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LENGTH: 871 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY:
CLOME: Consensus
US-08-744-026-2
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US-08-744-026-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPAX: 415-85-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEVENT CALLETY TO THE TOTAL TO THE TOT
                                                                                                                                                                                   Query Match 50.7%;
Best Local Similarity 89.0%;
Matches 737; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskette
COMPUTER: IDS COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: A NOVEL PROSTATE-SPECIFIC
TITLE OF INVENTION: KALLIKREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: US
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US-08-148-910-2

US-08-148-910-3

US-08-148-910-13

US-08-148-910-14

US-08-448-937A-3

US-08-448-937A-3
                                                                                                                                                                                   Score 641; DB 3; 1
Pred. No. 5.6e-153;
0; Mismatches 8;
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Sequence 2, Appli
Sequence 3, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
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Result

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Score 641

Match

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Scoring table:

Searched:

Issued_Patents_NA:*

176461 segs, 45838279 residues

Title: Perfect score:

US-09-030-606-173 1265 1 GGCAGCCCGCACTCGC

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nucleic search, using sw model

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US-07-914-281-5/c
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                                                                                                                  GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLLPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                           ZIP: 22202
COMPUTER READABLE FORM:
                                                                 ADDRESSEE: OBLON,
ADDRESSEE: P.C.
STREET: 1755 Jeff
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                      787
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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US-08-393-246-5/c; Sequence 5, Application US/08393246; Patent No. 5555900; GENERAL INFORMATION:
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US-07-914-281-5
                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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APPLICATION NUMBER: US/07/914,
FILING DATE: 1920720
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LAVALLEY, Jean-Paul M.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)466-2347
TELEFAX: 248855 OPAT UR
TELEFAX: 248855 OPAT UR
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 base pairs
TYPE: NUCLEIC ACID
CTP ANDEDNESS: in KROWN
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Best Local Similarity
Matches 272; Conserv
ADDRESSEE: OBLON, SPIN
ADDRESSEE: P.C.
STREET: 1755 Jefferson
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
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TOPOLOGY: unk
MOLECULE TYPE:
                                                                                                                                                                          APPLICANT: LOWE, JOHN B.

APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE IS

TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
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                                                                                                                  1755 Jefferson
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  Floppy disk
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                                                                                                                    Davis Highway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 184.6; DB 1; Length 8174; Pred. No. 9.2e-38; 0; Mismatches 64; Indels 12;
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                                                                                                                      Fourth
                                                                                                                                                          MAIER & NEUSTADT
                                                                                                                      Floor
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US-08-525-058A-5/c
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REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-!
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEPAX: (703)486-2347
TELEY 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENCTH: 8174 base pairs
TYPE: nucleic acid
                                                                                                                                         Sequence 5, Application US/08525058A Patent No. 5770420 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                          APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            1086 CCAGAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCCAGNGGTCCAA 1133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                            -CCCAGACCCTCCTCAGACCCAGGAGTCCAGGCCCCCACCCCTCCTCCTCAGAC
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 OBLON, SPIVAK,
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Pred. No. 9.2e-38;
0; Mismatches 64;
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McCLELLAND,
 MAIER
NEUSTADT,
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                                                                                                    Sequence 3, Application PC/TUS9100899
GENERAL INFORMATION:
APPLICANT: Lowe, John B.
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Best Local Similarity
Matches 272; Conserv
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TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 base pairs
           TITLE OF INVENTION: Method and Products For the Synthesis of TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolip TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned TITLE OF INVENTION: Genetic Sequences That Determine These Structur NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8174 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CITY: Arlington
STATE: Virginia
T S.A.
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CORRESPONDENCE ADDRESS:
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ZIP: 22202
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ER: 2363-060-55
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RESULT 6
US-08-308-949A-1/c
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LOCATION: 4686.5780
; OTHER INFORMATION: /lai
PCT-US91-00899-3
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Best Local S
Matches 272
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ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Ph.D., Jean-P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-5940
TELEFAX: (703)486-2347
TELEFAX: (703)486-2347
TELEFAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 Dase pairs
TYPE: NUCLEIC ACID
STRANDENESS: (NAME)
                                                                                                                                                                           1026
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: .19910214
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ADDRESSEE:
STREET: 17:
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TISSUE TYPE:
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STATE: Virginia
ZIP: 22202
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les 272; Conserv
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                                                                                                    CCAGAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAA 1133
                                                                  CCAGGAGTCCAGACCCCCAGCCCTCCCTCAGACACAGAAGGCCTA 681
                                                                                                                                                                         CCCCAACCCCTCCTTCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGAC 108:
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                                                                                                                                       1755 Jefferson Davis Highway, Suite 400
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Pred. No. 9.2e-38;
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Sequence 1/ Application US/08308949A

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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,949A
FILING DATE: September 20, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/947,127
FILING DATE: September 27, 1992
APPLICATION NUMBER: 07/947,127
FILING DATE: September 27, 1992
APPLICATION NUMBER: 33,542
REGISTRATION NUMBER: 33,542
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GENERAL INFORMATION:
APPLICANT: Kotin, Robert M.
APPLICANT: Berns, Kenneth I.
APPLICANT: Linden, Ralph M.
TITLE OF INVENTION: Human Adeno-Associated Virus Integration
TITLE OF INVENTION: Site DNA and Uses Thereof
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.5%;
Best Local Similarity 72.5%;
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                        1105 CCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCAC 1139
                                                                                                                                                                                                                                                                         3823 G--GCCCCAGCCCTCCTCCCTCGGACCCAGGAGTCCAGGCCCCCAGTCCCTCCACCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3940 GGAGTCCAGGCCCCCAGCCTCTCCCCATTCAGACCCAGGGGTCCAG----GCCCAGCCCCG 3884
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                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCTCCTCTCAAACCCAGGAGCCCAGGCCCCC 3672
                                                                                                                                                                                                           AGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGACCCAGAGGTNNAGGTCCCAG 1104
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Pred. No. 6.2e-28;
0; Mismatches 78
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RESULT 8
PCT-US96-04294-1/c
; Sequence 1, Application PC/TUS9604294
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,395
FILING DATE: 22-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X8350A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEPHONE: 317-277-1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.4
Best Local Similarity 61.3
Matches 171; Conservative
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APPLICANT: Dixon, Eric P.

APPLICANT: Johnstone, Edward M.

APPLICANT: Little, Shella P.

APPLICANT: Little, Shella P.

APPLICANT: No. 5733768ris, Franklin H.

TITLE OF INVENTION: PROTEASE AND RELATED DNA COMPOUNDS NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ell Lilly and Company

STREET: Lilly Corporate Center/Patent Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Lilly Corpo
CITY: Indianapolis
STATE: Indiana
COUNTRY: United Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 TGCCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGGTGTCTGAGGAAGGTCTGCAGTAAGC 516
                                                                                                                                                                                                                                                                                                                                          572 ATTCCTGCCAGGGTGATTCTGGGGGTCCGCTGGTATGTGGAGACCACCTCCGAGGCCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 TCCCTGACACCATCCAGTGTGCATACATCCACCTGGTGTCCCCGTGAGGAGTGTGAGCATG 511
                                                                                                                                                                      692
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                    ACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTG 636
                                                                                                                                                                                                                                                                                TGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCCAACCTCT 696
                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTACCCTGGCCAGATCACCCAGAACATGTTGTGTGCTGGGGATGAGAAGTACGGGAAGG 571
                                                                                                                                                                                                             GCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCA 735
                                                                                                                                                                                                                                                       TGTCATGGGGTAACATCCCCTGTGGATCAAAGGAGAAGCCAGGAGTCTACACCAACGTCT
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                           PCT-US96-04294-3/c; Sequence 3, Application PC/TUS9604294; GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
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Best Local Similarity 59.8
Matches 162; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04294
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEPAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER: US 08,
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,08
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 1089 base pairs
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CORRESPONDENCE ADDRESS:
ADDRESSE: E11 Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
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APPLICANT: Little, Sheila P.
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                               378
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                     GCAAATTCACTGAGTGGATAGAGAAAACCGT 727
                                                                    TGTCCTGGGGAACTTTCCCTTGCGGCCAACCCCAATGACCCAGGAGTCTACACTCAAGTCT
                                                                                                                                                                                                                                                                                         TTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGG 439
GCAAGTTCACCAAGTGGATAAATGACACCAT 228
                                                                                                         TGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCT
                                                                                                                                           ACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTG
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59.8%; Pred. No. 7.3e-16;
rative 0; Mismatches 109;
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US-08-557-146-1
; Sequence 1, Application US/08557146
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                                                                                                                                           RESULT
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; MOLECULE TYPE:
PCT-US96-04294-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.6
Best Local Similarity 59.8
Matches 162; Conservative
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APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K,
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: x9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-10190
                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Little, SITITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
      APPLICANT: Egelrud, Torbjorn APPLICANT: Hansson, Lennart TITLE OF INVENTION: Recombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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STATE: Indiana
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                         GCAAATTCACTGAGTGGATAGAGAAAACCGT 727
                                                                                                                                                                                                                                                                                                                                                        ACGCCTGCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGG
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                                                                                                                                                                                                   GCAAGTTCACCAAGTGGATAAATGACACCAT 228
                                                                                                                                                                                                                                                                              TGTCCTGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTCT
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                                                                                                                                                                                                                                                                                                                    TGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCT 696
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317-276-3861
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AMYLOID PRECURSOR PROTEIN PROTEASE AND
RELATED NUCLEIC ACIDS
Lennart
Recombinant Stratum Corneum Chymotryptic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1089;
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US-08-557-146-1
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                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 354-81 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/57,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enzyme (SCCE) NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 986 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                     457 TGCCTACCGTGCTGCAGTGCGTGAACGTGTCCGGTGGTGTCTGAGGAGGTCTGCAGTAAGC 516
                                                                                                                                   620
 740
                                                                  089
                                                                                                                                                    577 ACTCCTGCAACGGTGACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTG
                                                                                                                                                                                                 560 TTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAA 619
                                                                                                                                                                                                                                   517 TCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGACCAGAAGG 576
                                                                                                                                                                                                                                                                  500 TTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGG 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
GCAAGTTCACCAAGTGGATAAATGACACCAT
                   GCAAATTCACTGAGTGGATAGAGAAAACCGT
                                                                                                TGTCTTTCGGAAAAAGCCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCT 696
                                                              TGTCCTGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGT
                                                                                                                               ACGCCTGCAATGGTGACTCAGGGGGACCGTTGGTGCAGAGGTACCCTGCAAGGTCTGG
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                                                                                                                                                                                                                                                                                                                                      Conservative
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25..786
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SYSTEM: PC-DOS/MS-DOS
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112..783
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25..90
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Pred. No. 1.8e-15;
0; Mismatches 110;
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770
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.98;
Best Local Similarity 53.98;
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Patent No. 584087
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/79
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
TITLE OF INVENTION: KALLIKRBIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                        530 GTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGACCAGAAGGACTCCTGCAACGG 589
                                                                                                                                                                                                                                                                                                                                                                             470 GCAGTGCGTGAACGTGTCGGTGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGACCCGCT 529
                                                                                                                                                                                                                                                                                                                                                                                                                       578 CATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGCAAGGACTCCTGCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 CTGCCCAGTCGCGGGGCTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCT 469
758 CTGGATCCAGGAGACGATGAAGAACAATTA 787
                                                                                                                                                                                                        590 TGACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAA 649
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CITY: Palo Alto
STATE: CA
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                                                                             GATCCGTGTGCGATCACCCGAAAGCCTGGTGTTACACGAAAGTCTGCAAATATGTGGA 757
                                   GTGGATAGAGAAAACCGTCCAGGCCAGTTA 739
                                                                                                                                                                TGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATCTCCTGGGGCCA 697
                                                                                                                                                                                                                                                                                                                                     GCGATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAGAACGCCTACCCCGGCAA 577
                                                                                                                         AGCCCCGTGTGGCCAAGTTGGCCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGA 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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US-08-738-413B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Agkistrodon halys brevicaudus
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MOLECULE TYPE: (
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 699 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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661 A 661
                                                                                               660 GGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAG 719
                                                                                                                                                                                                  481 AGAACATTGTGTGCAGGTATCCTGGAAGGAGGCAAAGATTCATGTAACGGTGACTCTGGG 540
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ZIP: 10022
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5.8%; Score 73.8; DB 3;
Local Similarity 63.0%; Pred. No. 3.5e-10;
nes 114; Conservative 0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-753-6237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
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                                                                                                                                GGACCCCTCATCTGTAATGGACAATTCCAGGGCATTGCATATTGGGGGGGCCGATACTTGT
                               A 720
                                                               GGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCCGTGT 659
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OTHER INFORMATION: codes for the protein of SEQ ID NO: 6
US-08-684-862-11
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,040
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: PCT/EP91/01361
FILING DATE: 19-UUL-1991
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                Matches 118;
                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 957 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect version 5.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb sto
COMPUTER: IBM AT-compatible, 80286 processor
OPERATING SYSTEM: MS-DOS version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Kell & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NO. 575
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bach, AIII
APPLICANT: Hillen, He
APPLICANT: Bialojan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                             641
854 TTATAATGACTGGATCAACA 873
                                      701 ATTCACTGAGTGGATAGAGA 720
                                                                                                                                                                                 581 CTGCAACGGTGACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTC 640
                                                                                                                                                                                                                      674 TGAGGTGCTGGCAGAATACAGAACATTGTGTGCAGGTATCGTGCAAGGAGGCAAAGATAC 733
                                                                                                                                                                                                                                                          Local Similarity 59.(
les 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                        TTATGGGGCGCATCCTTGTGGCCAACCTCTTAAGCCTGGTATCTACACCAGGCTCCATGA 853
                                                                                                           TTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAA 700
                                                                                                                                               ATGTATGTATGACTCTGGAGGACCTCTCATCTGTAATGAACAAGTCCAGGGCATTGTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                210 to 911
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Pred. No. 7.1e-09;
0; Mismatches 82
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US-08-232-463-14
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US-08-232-463-14
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNEK, E.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
1029 CAACCCCTCCTTCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGACCCA 1088
                              IMMEDIATE SOURCE:
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ADDRESSEE: Foley & Lardner
                                                                                                                       909 AGGAGTCCAGACCCCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGCCCCTCCTCCNT 968
                                                                                                                                                                                Local Similarity. 2.3%; nes 9; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22313-0299
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                                                          CAGACCCAGGAGTCCAGACCCCCCAGCCCCTCCTCCCTCAGACCCAGGGGTTGAGGCCCC 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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Pred. No. 6.5e-08;
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; MOLECULE TYPE:
US-08-467-155A-2
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US-08-467-155A-2
                                                                                                                                                                                                                                                                                         Query Match 5.2%;
Best Local Similarity 54.9%;
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,155A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1454 base pairs
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APPLICANT: Band, Vimla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FITLE OF INVENTION:
                                                                                            631 GCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGGCCAAGTTGGCGTGCCAGGTGTCTACACCA 690
                                                                                                                                                                    571 AGAAGGACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGG 630
                                                                                                                                               743 GCCAGGACCCTTGCCAGAGTGACTCTGGAGGCCCCCTGGTCTGTGACGAGACCCTCCAAG 802
                                                                                                                                                                                                                   683 GTGAGGTCTTCTACCCTGGCGTGGTCACCAACAACATGATATGTGCTGGACTGGACCGGG 742
                                                                                                                                                                                                                                                       511 GTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGGGGGAGGGGCAAGACC 570
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CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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ZIP: 02110-2804
GCATCCTCTCGTGGGGTGTTTACCCCTGTGGCTCTGCCCCAGCATCCAGCTGTCTACACCC
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linear
PE: cDNA
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                                                                                                                                                                                                                                                                                         Score 65.4; DB 3; Length 1454;
Pred. No. 5.7e-08;
0; Mismatches 106; Indels 0
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Search completed: September 25, 1999, 07:29:29 Job time: 3406 sec

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Database :
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Sequence:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1265
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Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/5D_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCTUS9_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/packfiles1.seq:*
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    GGCAGCCCGCACTCGCAGCC.....AGAGANGNGCAAAAAAAAA 1265
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 US-08-744-026-2
US-08-7914-281-5
US-08-32-246-5
US-08-39-32-46-5
US-08-361-395-2
PCT-US96-04294-1
PCT-US96-04294-1
PCT-US96-04294-1
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US-08-684-862-11
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US-08-684-862-11
US-08-684-862-12
US-08-684-862-13
US-08-684-862-13
US-08-684-862-13
US-08-684-024-1
US-08-685-0-129-1
US-08-650-129-3
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(without alignments)
720.047 Million cell updates/sec
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Compugen Ltd.
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 sequence
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		atc cal	ADDRESSEE: INCYTE PHARMACEUT STREET: 3174 POTTET DIVE CITY: Palo Alto STATE: CA COUNTRY: US ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATION SYSTEM: DOS SOFTWARE: FASTSEQ Version 2. CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/74 FILLING DATE: Herewith CLASSIFICATION DATA: APPLICATION DATA: APPLICATION UMBER: 314 PRIOR APPLICATION DATA: APPLICATION UMBER: 36,749 REFERENCE/DOCKET NUMBER: 9F TELEFOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-85-0555 TELEFAX: 415-85-0555 TELEFAX: 415-85-055 TELEFAX: 415-85-016 STRANDEDNESS: single TOPOLOGY: Linear IMPEDIATE SOURCE: LIBRARY: CLONE: Consensus 08-744-026-2			44444. 00000000	
TGCATO TGCATO	CGCAGC	h Similarity 37; Conservat	EE: INCYTE 3174 POTTE PAID ALTO CA 3174 POTTE PAID ALTO CA TYPE: Disk TYPE: Disk TYPE: Disk TYPE: Disk TYPE: Disk TION NUMBER TON NUMBER TON NUMBER TON NUMBER TON TINFOR TON TINFON	pplication 86148 RMATION: RMATION: GO11, Su NVENTION: NVENTION: SEQUENCES: SEQUENCES:			
CGCAGTO	CCTGGC	50.7 89.0 cvative	BEE: INCYTE PHARMAC 3174 POTTET PHARMAC 3174 POTTET PHARMAC 3304 4304 4304 READABLE FORM: TYPE: Diskette TYPE: Diskette TYPE: Diskette TYPE: Diskette TYPE: DATA: TION NUMBER: DOS RE: PASTSEQ Version REALTION NUMBER: US/08, DATE: Herewith FIGATION NUMBER: US/08, TICATION DATA: TICATION DATA: TICATION NUMBER: 36,7 MACHINION DATA: TINFORMATION: Billings, Lucy J RATION NUMBER: 36,7 REALTION NEORMATION NE: 415-855-0555 CHARACTERISTICS: CHARACTERISTICS: REALTION NUMBER: BILLINGS FOR SEQ ID NO: 2: CHARACTERISTICS: REALTION NUMBER: REALTION NOTERISTICS: REALTION NUMBER: REALTION NOTERISTICS: REALT NOTERISTICS: REALTION NOTERISTICS: REALTION NOTERISTICS: REALTI	2 Application US/08744026 5786148 5786148 TEORMATION: TI: Bandman, Olga GOli, Surya VE. INVENTION: A NOVEL PRO 'INVENTION: KALLIKREIN P SEQUENCES: 5 NDERCE ADDRESS:		12001 329 970 329 2033 329 2033 329 970	
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GCTGT	GGCAC FFFF GGCAC	Score Pred. 0; Mi	PHARMACEUTICALS r Drive tte atible atible DOS Version 2.0 ATA: US/08/744,026 1th A:	4026 PROSTATE	AL	08-08 08-08 08-08 08-08 08-08 08-08 08-08	
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GTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTTTCCAGAACTCCTACACC 	CCGCACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTGCTCGGGC 	DB 3; 6e-153; s 8;	INC.	SPECIFIC	STNIS	-08-458-568A-11 -08-148-910-2 -08-148-910-3 -08-148-910-13 -08-148-910-14 -08-448-937A-2 -08-448-937A-3 -08-448-937A-13	
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RESULT 2
US-07-914-281-5/c
US-07-914-281-5/c
; Sequence 5, Application
; Patent No. 5324663
; GENERAL INFORMATION:
; APPLICANT: LOWE, JC
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                                                                                                TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                           COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                               CGGAAGGAATTCAGGAATATCTGTTCCCAGCCCTCCTCCTCCTCAGGCC 834
                                                                                                                                                                                                                                                                                                                                                                                                  TCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCAAATACATCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGGCCAAG
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RESULT 3
US-08-393-246-5/c
US-08-393-246-5/c
Sequence 5, Application US/08393246
Patent No. 5595900
Patent N
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NAME: Lavalleye, Jean-Paul M. P.

REGISTRATION NUMBER: 31,451

REFERENCE/DOCKET NUMBER: 2363-00

TELECOMMUNICATION INFORMATION:

TELEPAN: (703)521-4500

TELEPAN: (703)46-2347

TELEX: 24885 OPAT UR

INFORMATION FOR SEQ ID NO: 5:
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Best Local Similarity 78.2%;
Matches 272; Conservative
STREET: 1755 Jefferson CITY: Arlington STATE: Virginia COUNTRY: U.S.A. ZIP: 22202 COMPUTER READMBLE FORM: MEDIUM TYPE: Floppy d.
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LENGTH: 8174 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic
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APPLICATION NUMBER:
FILING DATE: 19920
CLASSIFICATION: 53
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Pred. No. 9.2e-38;
0; Mismatches 64;
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RESULT 4
US-08-525-058A-5/c
US-08-525-058A-5/c
; Sequence 5, Application U;
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHE
; INVENTION: 1)
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Best Local S
Matches 272
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APPLICATION NUMBER: US 08/220,433

FILING DATE: 30-MAR-1994

APPLICATION NUMBER: US 07/914,281

FILING DATE: 20-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lavelleye, Jean-Paul M. P.

REGISTRATION NUMBER: 31,451

REFERENCE/DOCKET NUMBER: 2363-060-5

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION JAPAGE-3417
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 base pairs
APPLICANT: LOWE, JOHN B
TITLE OF INVENTION: METI
TITLE OF INVENTION: GLY
TITLE OF INVENTION: GF OF
TITLE OF INVENTION: GF OF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPI
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
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Local Similarity 78.2%;
nes 272; Conservative
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DEDNESS: unknown
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                                                                                                                         ЈОНИ В.
                                  METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
23
     SPIVAK,
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Pred. No. 9.2e-38;
0; Mismatches 64;
   MCCLELLAND,
   MAIER
   & NEUSTADT,
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                                                                                                                                                                RESULT 5
PCT-US91-00899-3/c
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                         Sequence 3, Application PC/TUS9100899 GENERAL INFORMATION:
APPLICANT: Lowe, John B.
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Best Local Sim
Matches 272;
               TITLE OF INVENTION: Method and Products For the Synthesis of TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids, TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned TITLE OF INVENTION: Genetic Sequences That Determine These Structur NUMBER OF SEQUENCES: 16
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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 CORRESPONDENCE
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                                                                                                                                                                                                                                                                                                             CCCCAACCCCTCCTCCTCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGAC 1085
                                                                                                                                                                                                                                                                                                                                                                                                       CNTCAGACCCCAGGAGTCCAGACCCCCAGGCCCTCCTCCTCAGACCCAGGGGTTGAGGC 1025
                                                                                                                                                                                                                                        CCAGGAGTCCAGAGCCCCAGCCCTCCTCCTCAGACACAGAAAGGCCTA
                                                                                                                                                                                                                                                                                                                                                                                      CCTCAGACCCAGGAGCCCAAGTTCCCCAGCCCCTCCTCAGATCCAGGAGTACAGG-787
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ADDRESS:
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78.2%;
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RESULT 6
US-08-308-949A-1/c
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; LOCATION: 4686..5780
; OTHER INFORMATION: /lai
PCT-US91-00899-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: LAVALLEYPE Ph.D., Jean-PR
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-5940
TELEFAX: (703)466-2347
TELEFAX: (703)466-2347
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
Sequence 1, Application US/08308949A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: 19910214
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                   1025 ACTTAGGAGTCCAGGCTCCCGGCCCTCCTTCCTCAGACCCAGGAGTCCAAGCCCCCTGC 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
                                                                                                                          1086 CCAGAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAA 1133
                                                                                                                                                                               1026 CCCCAACCCCTCCTCCTCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGAC 1085
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                                                                                                                                                                                                                                                966 CNTCAGACCCAGGAGTCCAGACCCCCCAGCCCCTCCCTCAGACCCCAGGGGTTGAGGC 1025
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                                                                                          CCAGGAGTCCAGAGCCCCAGCCCTCCTCCCTCAGACACAGAAGGCCTA 681
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                                                                                                                                                           il Similarity
272; Conserv
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Pred. No. 9.2e-38;
0; Mismatches 64;
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GENERAL INFORMATION:
APPLICANT: Kotin, Robert M.
APPLICANT: Berns, Kenneth I
APPLICANT: Linden, Ralph M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 243; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/947,127
FILING DATE: September 27, 1992
ATTORNEY/AGENT INFORMATION:
NAME: CAITOIL, Alice 0.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC92-10;
TELECHONE: 617-861-6240
TELEPHONE: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATEN: COMPATEN: COMPATEN: COMPATEN: COMPATEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                               3883
                                                                                                                                                                                                                                                                                                        3940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/308,91
FILING DATE: September 20, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human Adeno-Associated Virus Integration TITLE OF INVENTION: Site DNA and Uses Thereof NUMBER OF SEQUENCES: 23
   3706
                                                                                                                                                                                                                                                                                                                                                                                 4000 CCCAACCCCTCCCCATTCAACCCAGGAGGCCCAGGCCCCTCCGGCCCTCAGATGAA 3941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4060 base pairs
                                                                                                                                                                                                                                                                    933
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CITY: L
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                 CCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCAC 1139
                                                                                                                                                  G--GCCCAGCCTCCTCCCTCGGACCCAGGAGTCCAGGCCCAGTCCCTCCACCCTC
                                                                                                                                                                                                                             GGAGTCCAGGCCCCCAGCCTCTCCCCATTCAGACCCAGGGGTCCAG----GCCCAGCCCCG
CCCCTCCTCTCAAACCCAGGAGCCCAGGCCCCC 3672
                                                                                                            AGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGACCCAGAGGTNNAGGTCCCAG 1104
                                                                                                                                                                                     GACCCCCCAGCCCCTCCTCCCTCAGACCCAGGGGTTGAGGCCCCCAACCCCTCCTTC 1044
                                                                                                                                                                                                                                                                CCTCCCTCAGACCCAGGAGTCCAG------CCCCTCCTCCNTCAGACCCAGGAGTCCA 984
                                                                       AGACCCAGGAGTCC-AGGCCCCAGCCCTCCTCCCTCGGACCCAGGAGTCCAGGCCCCAG
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DEDNESS: single
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72.5%;
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Pred. No. 6.2e-28;
0; Mismatches 78;
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RESULT 8
PCT-US96-04294-1/c
; Sequence 1, Application PC/TUS9604294
; GENERAL INFORMATION:
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Best Local Similarity 61.3%;
Matches 171; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361/395
FILING DATE: 22-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X8350A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5733768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
APPLICANT: No. 5733768ris, Franklin H.
TITLE OF INVENTION: PROTEASE AND RELATED DNA COMPOUNDS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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LENGTH: 732 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                       452
                                                                                                                                                                                                                                                                    517 TCTATGACCCGCTGTACCACCCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                          457 TGCCTACCGTGCAGTGCGTGAACGTGTCGGTGGTGTCTGAGGAGGTCTGCAGTAAGC 516
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CITY: Indianapolis
STATE: Indiana
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ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCTGACACCATCCAGTGTGCATACATCCACCTGGTGTCCCCGTGAGGAGTGTGAGCATG 511
                                                                                                                         GCAGATACACGAACTGGATCCAAAAAACCATTCAGGCCA
                                                                                                                                                            GCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCA 735
                                                                                                                                                                                              TGTCATGGGGTAACATCCCCTGTGGATCAAAGGAGAGCCAGGAGTCTACACCCAACGTCT
                                                                                                                                                                                                                                  TGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCT
                                                                                                                                                                                                                                                                                                                                             CCTACCCTGGCCAGATCACCCAGAACATGTTGTGTGCTGGGGATGAGAAGTACGGGAAGG
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Lilly Corporate Center/Patent Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 317-277-1090
317-276-3861
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Pred. No. 2.5e-18;
0; Mismatches 108;
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RESULT 9
PCT-US96-04294-3/c
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Best Local Similarity
Matches 162; Conserv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                         438
                                                                                                                   697
                                                                                                                                                      318
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                                                                              258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                 GCAAATTCACTGAGTGGATAGAGAAAACCGT 727
                                                                                                                                                                                                                                                                                                       TITACAAGGACTIACIGGAAAATICCAIGCIGIGCGCIGGCAICCCCGACICCAAGAAAA 379
                                                                                                                                                                                                                                                                                                                                                                                 TTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGG 439
                                                                                                                                                                            TGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCT
                                                                                                                                                                                                                                                                                                                                        TCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGG 576
                                                                              GCAAGTTCACCAAGTGGATAAATGACACCAT 228
                                                                                                                                                    TGTCCTGGGGAACTTTCCCTTGCGGCCAACCCCAATGACCCAGGAGTCTACACTCAAGTCT
                                                                                                                                                                                                                               ACGCCTGCAATGGTGACTCAGGGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGG
                                                                                                                                                                                                                                                                ACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTG 636
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Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1089;
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                                                                                                                                                                                         696
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Sequence 3, Application PC/TUS9604294 GENERAL INFORMATION:

Dixon, Eric P.

Johnstone, Edward

APPLICANT:

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US-08-557-146-1
; Sequence 1, Application US/08557146;
; Patent No. 5834290;
; Patent No. 5834290;
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF, INVENTION: Recombinant
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                                                                                                                                          RESULT 10
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TOPOLOGY: linear
MOLECULE TYPE: mRNA
PCT-US96-04294-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.6%;
Best Local Similarity 59.8%;
Matches 162; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION UNMBER: 38,082
REFERENCE, DOCKET NUMBER: 923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEPHONE: 317-276-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Little, Shei
TITLE OF INVENTION: REI
TITLE OF INVENTION: REI
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
COMPUTER: FOC COMPATIBLE
COMPUTER: PACENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
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                                                                                                                                                                                                    258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                GCAAGTTCACCAAGTGGATAAATGACACCAT 228
                                                                                                                                                                                                                            GCAAATTCACTGAGTGGATAGAGAAAACCGT 727
                                                                                                                                                                                                                                                                         TGTCCTGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTCT
                                                                                                                                                                                                                                                                                                                                                    TGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCT 696
                                                                                                                                                                                                                                                                                                                                                                                          ACTCCTGCAACGGTGACTCTGGGGGGCCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTG 636
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                                                                                                     Application US/08557146
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Lilly Corporate Center
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VENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
VENTION: RELATED NUCLEIC ACIDS
     Lennart Recombinant Stratum Corneum Chymotryptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT/US96/04294
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Pred. No. 7.3e-16;
0; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-557-146-1
                                                                                                                                                                                                                                                                                                                                              Matches 161;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 986 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION UNMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                      620
                                                                                                                                                                                                                                                                                                         457 TGCCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGGTGTCTGAGGAGGTCTGCAGTAAGC 516
                                                                                                                                                                  577 ACTCCTGCAACGGTGACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTG 636
                                                                                                                                                                                                        560 TTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAA 619
                                                                                                                                                                                                                          517 TCTATGACCCGCTGTACCACCCCAGCAGGTTTCTGCGCCGGCGGAGGGCAAGACCAGAAGG 576
                                                                                                                                                                                                                                                                          500 TTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGG 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 14-DEC-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: .nucleic acid
                   GCAAATTCACTGAGTGGATAGAGAAAACCGT
GCAAGTTCACCAAGTGGATAAATGACACCAT 770
                                                                                                TGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCT 696
                                                                TGTCCTGGGGAACTTTCCCTTGCGGCCAACCCCAATGACCCCAGGAGTCTACACTCAAGTGT
                                                                                                                                  ACGCCTGCAATGGTGACTCAGGGGGACCGTTGGTGCTGCAGGGTACCCTGCAAGGTCTGG
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25..786
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SYSTEM: PC-DOS/MS-DOS
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112..783
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25..90
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                                                                                                                                                                                                                                                                                                                                                             7.58;
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                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                           Score 95; DB 4; Le
Pred. No. 1.8e-15;
0; Mismatches 110;
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                                727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,137
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: GOIL, SURYA K.
APPLICANT: GOIL, SURYA K.
TITLE OF INVENTION: A NOVEL PROSTATE ASSOCIATED
TITLE OF INVENTION: KALLIKREIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-790-137-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0195 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415-855-0555
  758 CTGGATCCAGGAGACGATGAAGAACAATTA 787
                                                                                                                                                                                                                                                  578 CATCACAGACACCATGGTGTGCCCAGCGTGCAGGAAGGGGGCAAGGACTCCTGCCAGGG
                                                                                                                                                                                                                                                                                       530 GTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGACCAGAAGGACTCCTGCAACGG 589
                                                                                                                                                                                                                                                                                                                                   518 GCGATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAGAACGCCTACCCCGGCAA 577
                                                                                                                                                                                                                                                                                                                                                                            470 GCAGTGCGTGAACGTGTCGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGACCCGCT 529
                                                                                                                                                                                                                                                                                                                                                                                                                      410 CTGCCCAGTCGCGGGGGCTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCT 469
                                                                                                                                                                                                           590 TGACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAA 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 94304
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STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                  GTGGATAGAGAAAACCGTCCAGGCCAGTTA 739
                                                                                                                                                             TGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATCTCCTGGGGCCA
                                                                                   GGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAATATGTGGA
                                                                                                                          AGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 86.8; DB 4; Length 833; Pred. No. 2e-13; O; Mismatches 152; Indels
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US-08-738-413B-8
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                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNAL, ...

NAME: Ludwig, S. Peces.

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136

TELECOMMUNICATION INFORMATION:

METERPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: CHUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: lin
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 699 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Agkistrodon halys brevicaudus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A NOVEL CDNA OF DIRECT-ACTING TITLE OF INVENTION: FIBRINOLYTIC SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                            660 GGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAG 719
                                                                                                                              541 GGACCCCTCATCTGTAATGGACAATTCCAGGGCATTGCATATTGGGGGGGCCGATACTTGT 600
                                                                                                                                                                                                                             540 AGCATGTTCTGCGCCGGGGGGAGGGCAAGACCAGAAGGACTCCTGCAACGGTGACTCTGGG 599
661 A 661
                               720 A 720
                                                                                                                                                            600 GGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCCGTGT 659
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              Match 5.8%;
Local Similarity 63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/738,413B FILING DATE: October 23, 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Darby & Darby PC
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US
                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIM, Doo-Sik
YUN, Yung-Dae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HWANG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHUNG, Kwang-Hoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                              Score 73.8; DB 3;
Pred. No. 3.5e-10;
0; Mismatches 67;
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    Matches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-JUL-1991 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 957 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM AT-compatible, 8028
OPERATING SYSTEM: MS-DOS version
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,040
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: PCT/EP91/01361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillen, He APPLICANT: Bialojan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                             521 TGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGACCAGAAGGACTC 580
                                                                                                                                                                                                                        674 TGAGGTGCTGGCAGAATACAGAACATTGTGTGCAGGTATCGTGCAAGGAGGCAAAGATAC 733
                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 210 to 911
OTHER INFORMATION: the coding region shown in (2)(ix)(B)
OTHER INFORMATION: codes for the protein of SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                   ATTCACTGAGTGGATAGAGA 720
                                                                                                                                                  ATGTATGTATGACTCTGGAGGACCTCTCATCTGTAATGAACAAGTCCAGGGCATTGTATC 793
                                                                                                                                                                                   CTGCAACGGTGACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTC 640
TTATAATGACTGGATCAACA 873
                                                                        TTATGGGGGCGCATCCTTGTGGCCAACCTCTTAAGCCTGGTATCTACACCAGGCTCCATGA 853
                                                                                                           TTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08684862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillen, Heinz
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bach, Alfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agkistrodon rhodostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM AT-compatible, 80286 processor SYSTEM: MS-DOS version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keil & Weinkauf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                      5.4%;
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                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                    Score 68.8;
Pred. No. 7
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                  DB 3;
1e-09;
nes 82;
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US-08-232-463-14
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US-08-232-463-14
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Ap
Patent No. 5670
                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A
               1029 CAACCCCTCCTCCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGACCCA 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               849
                                                                                                                                                                                                                                                                               789 GAAGGAATTCAGGAATATCTGTTCCCAGCCCCTCCTCCTCAGGCCCAGGAGTCCAGGCC 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 26-AU
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ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                             CAGACCCAGGAGTCCAGACCCCCAGCCCCTCCTCCTCAGACCCAGGGGTTGAGGCCCC 1028
                                                                                                                                              AGGAGTCCAGACCCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGCCCCTCCTCCNT 968
                                                                                                                                                                             Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703)683-4109
                                                                                                                                                                                                                                                                                                                Conservative 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                             Score 66; DB 2;
Pred. No. 6.5e-08;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-467-155A-2
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US-08-467-155A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,155A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 00398/100001
                                                                                                                                                                                                                                                                                                                   Query Match 5.2%; Score 65.4; DB 3; Length 1454; Best Local Similarity 54.9%; Pred. No. 5.7e-08; Matches 129; Conservative 0; Mismatches 106; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08467155A Patent No. 5736377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1412 YYYYYYYYYYYYYYYYYYYY 1435
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1149 CCCTGNACACAGTGCCCCCTTGTG 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1089 GAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCCACCTAGATTTT 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 225 F
CITY: Boston
STATE: MA
                                                                                                                                                     691 ACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAACTCTG 745
                                                                          803 GCATCCTCGTGGGGTGTTTACCCCTGTGGCTCTGCCCAGCATCCAGCTGTCTACACCC
                                                                                                              631 GCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCA 690
                                                                                                                                                                                                                       511 GTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGACC 570
863 AGATCTGCAAATACATGTCCTGGATCAATAAAGTCATACGCTCCAACTGATCCAG 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vimla
                                                                                                                                                                                                                                                                                                               0; Mismatches 106; Indels 0; Gaps
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Search completed: September 28, 1999, 11:33:30 Job time: 2090 sec

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Search information block:
Query: US-09-030-606-173
Query: length: 1265
Database: PIR_60:*
Database sequences: 122810
Database length: 40065486
Search time (sec): 182.540000
       Pirl: TRBOTR
pirl: EGMSB
pir2: A25006
pir2: S49489
pirl: A25852
pirl: TRPGTR
pirl: TRRT1
pirl: TRMSM5
pirl: KOMS1
pirl: KOMS1
pirl: KOMS1
pirl: B2538
pir2: B31378
pir2: S31779
                                                                                                                                                                                                                                                                                                 pir2:S55067
pir2:JQ1471
pir2:S05494
pir1:KQRTP
pir2:S35711
pir1:KQRTTN
pir1:TRBOTR
                                                                                                                                                                                                                                                                                                                                                                                                                                         pir2:A29745
pir2:T01779
pir2:A41020
pir2:S33772
pir2:S55065
pir2:S55067
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pir2:A29745
pir2:T01779
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pir1:NGMSG
pir2:S5066
pir2:A29586
pir2:A31136
pir2:JE0236
pir2:JE0236
pir2:JE02371
pir2:A32297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pir1:TRDGC
pir2:S45303
pir2:B31136
pir2:A34079
pir2:A27547
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Sequence
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-MODEL-frame+_n2p.model -DEV=xlp
-Q-/Cgn2_1/USPTO_Spool/US09030606/runat_24091999_171617_29825/app_query.fasta.
-Q-/Cgn2_1/USPTO_Spool/US09030606/runat_24091999_171617_29825/app_query.fasta.
-DB-PIR_60 -QFWT-fastan -SUFFIX-rpr -GAPOP=12.000 -GAPEXT-4.000
-MINHATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -GGAPOP-6.000
-QGAPEXT-0.050 -XGAPOP-10.000 -YGAPEXT-0.500 -BEADOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-escore -ALIGN-15 -MODE-LOCAL
-GUTENT-Pfs -NORM-stat -USER-US09030606 -NCPU-6 -ICPU-3 -WAIT
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.6e-16
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       trypsin (EC 3.4.21.4) recours trypsin (EC 3.4.21.3) recurs trypsin (EC 3.4.21.4) - plaice tissue kallikrein (EC 3.4.21.3) recurs trypsin (EC 3.4.21.4) I precurs trypsin (EC 3.4.21.4) I precurs trypsin (EC 3.4.21.4) I precurs trypsin (EC 3.4.21.4) IV precurs trypsin (EC 3.4.21.4) precursor tissue kallikrein (EC 3.4.21.3) tissue kallikrein (EC 3.4.21.3) tissue kallikrein (EC 3.4.21.3) tissue kallikrein (EC 3.4.21.3) trypsin (EC 3.4.21.4) precursor trypsin (EC 3.4.21.4) precursor trypsin (EC 3.4.21.4) precursor trypsin (EC 3.4.21.4) I precursor trypsin (EC 3.4.21.4) I precursor trypsin (EC 3.4.21.4) [EC 3.4.21.3] tissue kallikrein (EC 3.4.21.3) tissue kallikrein (EC 3.4.21.3) procursor trypsin (EC 3.4.21.4) I precursor trypsin (EC 3.4.21.4) precursor trypsin (EC 3.4.21.4) I precursor trypsin (EC 3.4.21.4) precursor trypsin (EC 3.4.21.4) I precursor trypsin (EC 3.4.21.4) II precursor trypsin (EC 3.4.21.4) III precursor trypsin (E
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N:Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Sep-1998
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud,
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic en
A;Reference number: A53968
A;Accession: A53968
A;Accession: A53968
A;Accession: A53968
A;Accession: A53968
A;Roidcule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: GB:L33404; NID:g521214; PID:g532504
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A;Gene: GDB:PRSS6; SCCE
A;Gene: GDB:PRSS6; SCCE
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology <TRY>
F;30-245/Domain: trypsin homology <TRY>
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pir2:A35871
pir1:TRDFS
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to:
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                                                                                                                   342
                                                                        146
                                                                                                                                                                                         292 AGCATCAGCATTGCCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCCTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142
                            392 CCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGCTGACCCAGAGCTCT
                                                                                                                                                                                                                                                                                                                                                96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 rGlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrpValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 GlyAlaProCysAlaArgGlySerHisProTrpGlnValAlaLeuLeuSe
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                                                                                                                                                                                                                                                    AspThrLeu...GlyAspArgArg.....AlaGlnArgIleLysAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACAGTCTTGAGGCCGACCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAG
                                                                                                                   TTCTGGCTGGGGGTCTGCTGGCGAACGGTGAGCTCACGGGTGTGTCTGC
                                                                                                                                                                                                                                                                                                                                              rLysSerPheArgHisProGlyTyrSerThrGlnThrHisValAsnAspL
                                                                                                                                                                                                                                                                                                                                                                     CCTCTCCGTACGGCACCCAGAGTACAACAGACCCTTGCTCGCTAACGACC
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                                                                    lSerGlyTrpGly.....
                                                                                                                                                               LysValArgLeuProSerArgCysGluProProGlyThrThrCysThrVa
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41

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150 391 129

113

241

291

96 191 82 141 66 91 Length: Gaps:

247 5 42.915

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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-030-606-173 x I56559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 08-Sep-1997
C;Accession: 156559
R;Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishing J. Neurosci. 15, 5088-5097, 1995
A;Title: Expression activity-dependent changes of a novel limbic-serine protease gen A;Reference number: 156559; MUID:95348817
A;Accession: 156559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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                                                                                           157 GACCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCA 206
                                                                                                                                                                                           107 GTTTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 nValCysLysPheThrLysTrpIleAsnAspThrMetLys 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 rMetLeuCysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 CATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCCTGCAACGGTG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 IleSerProGlnAspCysThrLysValTyrLysAspLeuLeuGluAsnSe
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                                                                                                                                                                                                                                                                                           57 CTGCTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACT 106
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                                                                                                                                                                                                                                         ProHisSerGlnProTrpGlnAlaAlaLeuPheGlnGlyGluArgLeuIl 57
                                                ArgAspGlnPro...GluGlnGluIleGlnValAlaGlnSerIleGlnHi 106
                                                                                                                                             ysLysLysGlnLysTyrSerValArgLeuGlyAspHisSerLeuGlnSer 90
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2.851
71.311
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Gaps: 5
Percent Identity: 38.934
....CTCGCTAACGACCTCATGC 247
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106	sProCysTyrAsnAsnSerAsnProGluAspHisSerHisAspIleMetL 123	
248 123	TCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATC 297	
298 140	AGCATTGCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCCTCGTTTCTGG 347 :::::: :::	
348 156	CTGGGGTCTGCTGGCGAACGGTGAGCTCACGGGTGTGTGT	
398 159	CAAGGAGGTCCTCTGCCCAGTCGCGGGGGCTGACCCAGAGCTCTGCGTCC 447	
448 165	CAGGCAGAATGCCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGGTGTCT 497 ::: ::::: ::::: ::::: ::::: :::::	
498 181	GAGGAGGTCTGCAGTAAGCTCTATGACCCGGCTGTACCACCCCAGCATGTT 547 ::::: ::::: GlnAsnLysCysGluArgAlaTyrProGlyLysIleThrGluGlyMetVa 197	
548 197	CTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCCTGCAACGGTGACTCTG 597	
598 213	GGGGGCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGA 647 ::: 19G1yProLeuValCysAspGlyMetLeuGlnGlyIleThrSerTrpGly 229	
648 230	AAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTG 697 ::: :::	
698 246	CAAATTCACTGAGTGGATAGAGAAAACCGTC 728 :::::: ::: ::: sargTyrThrThrTrp1leLysLysThrMet 256	
seq_name:	: pir2:A44284 mentation block:	
seq_docum tissue ka N;Alterna C;Species C;Date: 1 C;Accessi	: (fragment) 1994 #text_change 29-	Jan-1999
Biochemis A; Title: A; Referen A; Accessi A; Status: A; Molecul	of rKlk10, a cDNA en	coding T-kininoge
A; Residue A; Cross-r A; Experim	es: 1-244 <ma1> references: GB:S48142; NID:g259430; PID:g259431 mental source: submandibular gland</ma1>	
A; Note: s R; Kato, H J. Bioche	(NCBIN:118095, NCBIF	118096) Iwanaga, S.
A; Title: A; Referen A; Accessi	s isolated from rat s	ubmaxillary gland:
A; Molecul A; Residue	e type: protein e type: protein es: 10-61 <kat></kat>	
C; Superfa C; Keyword F; 10-236/	amily: trypsin; trypsin homology ds: hydrolase; serine proteinase /Domain: trypsin homology <try></try>	

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alignment_block:
US-09-030-606-173 x A44284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: A44284 from: 1
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                                                                                                                            623
                                                                                                                                                                                                                                                   172
                                                                                                                                                                                                                                                                                                                                 155
                                                                                                                                                                                                                                                                                                                                                                         473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
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                                                                                                                                                                    189
                                                                                                                                                                                                    573 AAGGACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                           145 ProLeuAsnTrpGluLeu...........ProAspAspLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 GGGCTGACCCA.GAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCTGCA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 TCACGGGTGTGTCTGCCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 GGGGAACTCTTGCCTCGTTTCTGGCTGGGGTCTGCTGGCGAACGGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 IleThrAspGlyValLysValIleAspLeuProThrGluGluProLysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 TCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 GAGTCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 CAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 yrSerAsnTyrTyrHisValLeuLeuGlyArgAsnAsnLeuPheGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AsnSerGlnProTrpGlnValAlaIleIle.....AsnGluTyrLeuCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 CACTCGCAGCCCTGGCAGGCGCCACTGGTCATGGAAAACGAATTGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyGlyValLeuIleAspProSerTrpValIleThrAlaAlaH1sCysT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT
LysaspThrCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyVa 205
                                                                                                                                                                                                                                                                                                                          nCysValAsnIleHisLeuLeuSerAsnGluLysCysIleGluAlaTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...GluProPheAlaGlnTyrArgPheValAsnGlnSerPheProHisPr
                                                                                  lLeuGlnGlyIleThrSerTrpGlyAsnValProCysAlaGluProTyrA 222
                                                                                                                          CTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCCGTGTGGCCCAAGTTGGCG
                                                                                                                                                                                                                                              luGlnLysValThrAspLeuMetLeuCysAlaGlyGluMetAspGlyArg
                                                                                                                                                                                                                                                                                       ACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGACCAG
                                                                                                                                                                                                                                                                                                                                                                     GTGCGTGAACGTGTCGGTGTGTCTGAGGAGGTCTGCAGTAAGCTCTATG
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2.765
65.613
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Percent Identity:
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A.Cross-reference: GB:M11590; NID:g164096; PID:g164097
C.;Superfamily: trypsin; trypsin homology
C.;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymc
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <ENZ>
F:24-246/Product: trypsin, cationic #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:24-239/Domain: trypsin homology <TRY>
F:30-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted
F:33,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation:
A;Reference number: A26273; MUID:86284628
A;Accession: B26273
A;Molecule type: mRNA
A;Residues: 1-246 <PIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
trypsin (EC 3.4.21.4) precursor, cationic - dog
N;Alternate names: cationic trypsinogen
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change
C;Accession: B26273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-030-606-173 x TRDGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                       129 ProLysSerCysProAlaAlaGlyThrGlnCysLeuIleSerGlyTrpGl 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 ValMetLys 241
                                                             354 TCTGCTGGCGAACGGTGAGCTCACGGGTGTGTGTCTGCCCTCTTCAAGGA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 ACTGTTTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAG 15:
                                                                                                                                                                                                                                                                                                            254 AGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                   204 GCACCCAGAGTACAACAGACCCTTGCTCGCTAACGACCTCATGCTCATCA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 GCCGACCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 GTTCTGCTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCAC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 sPheCysGlyGlySerLeuIleAsnSerGlnTrpValValSerAlaAlaH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 SerArgAsnSerValProTyrGlnValSerLeu...AsnSerGlyTyrHi 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AGCCCGCACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATT
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gHisProArgTyrAsnAlaAsnThrIleAspAsnAspIleMetLeuIleL
                                                                                                                                                                                    isCysTyrLysSerArgIleGlnValArgLeuGlyGluTyrAsnIle...
                                                                                                                                                                                                                                               ysLeuSerSerProAlaThrLeuAsnSerArgValSerAlaIleAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaValSerGluGlyGlyGluGlnPheIleAsnAlaAlaLysIleIleAr
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2.737
68.163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 246
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Gaps:
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6
38.776
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145
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A; Molecule type: mRNA
A; Residues: 1-261 <GAU'>
A; Cross-references: EMBL:X75479; NID:g414018; PID:g414019
A; Cross-references: EMBL:X75479; NID:g414018; PID:g414019
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase
F; 1-24/Domain: signal sequence #status predicted <SIG>F; 25-261/Product: tissue kallikrein #status predicted <MAY
F; 25-253/Domain: trypsin homology <TRY>
F; 65,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
tlssue kallikrein (EC 3.4.21.35) precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Species: Canis lupus familiaris (dog)
C:Date: 20-oct-1994 #sequence_revision 03-Aug-1995 #text_change 17-Mar-1999
C:Accession: S45303; S38487
R:Gauthier, E.R.; Dumas, C.; Chapdelain, P.; Tremblay, R.R.; Dube, J.Y.
Biochim. Biophys. Acta 1218, 102-104, 1994
A:Title: Characterization of canine pancreas kallikrein cDNA.
A:Reference number: S45303; MUID:94250683
A:Accession: S45303
                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-030-606-173 x S45303
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uGlyTyrMetGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyP
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                                           TCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGAC 159
                                                                                            CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyCysAlaGlnLysGlyLysProGlyValSerProLysValCysLysTy
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leAsnAspAsnTyrGlnLeuTrpLeuGlyArgTyrAsnLeu...PheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTCCTCTGCCCAGTCGCGGGGGCTGACCCCAGAGCTCTGCGTCCCAGGCA 453
                                                                                                                                                                                                                       pir2:S45303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                      456.50
2.750
65.354
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A;Cross-references: GB:M19648; GB:J02837; NID:g205002; PID:g205004
A;Note: the authors translated the codon GTC for residue 230 as Cys
C;Superfamily: trypsin, trypsin home
C;Keywords: hydrodase; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-259/Product: tissue prokallikrein 3, submandibular #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - RyAlternate names: glandular prokallikrein 3, submandibular C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Mar-1990 *sequence_revision 31-Mar-1990 *text_chance;Roccession: B31136
                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-259 <CHE>
                                                                                                                                                                                                                                                                           A;Title: Molecular cloning and characterization of two rat renal kallikrein A;Reference number: A31136; MUID:89088074
A;Accession: B31136
                                                                                                                                                                                                                                                                                                                                                                                R;Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:B31136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisGluAspThrAlaGlnPheValGlnValArgGluSerPheProHisPr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGAGCCAGGGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGGCCTTGTGTCTTTCGGAAAAGCCCCCGTGTGGCCAAGTTGGCGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTCCTGCAACGGTGACTCTGGGGGGCCCCCTGATCTGCAACGGGTACTTG 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGACCAGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....ProAspLysPheIle.....TyrProAspAspLeuGlnCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGG 426
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alignment_block:
US-09-030-606-173 x B31136
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F;63,118,211/Active site: His, Asp, Ser #status predicted
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Percent Similarity:
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                               GCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAG 719
                                                                                                                                     GlyLysAspThrCysAsnGlyAspSerGlyGlyProLeuLeuCysAspGl
                                                                                                                                                                                                     isThrGlnMetValThrAspValMetLeuCysAlaGlyGluLeuGluGly 202
                                                                                                                                                                                                                                     ATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGAC
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                                                                                                                                                                                                                                                                                                                                         .....SerSerThrLysProLeuGluTrpGluPheProAspAspLe
                                                                  yValLeuGlnGlyIleThrSerTrpSerSerValProCysGlyGluThrA
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2.758
64.961
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Gaps:
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   252
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A;Molecule type: protein
A;Molecule type: protein
A;Rosidues: 25-43;112-138 <ELM>
A;Experimental source: submaxiliary gland
A;Note: 125-Lys was also found
C;Superfamily: trypsin; trypsin homology
C;Reywords: hydrolase; serine proteinase
F:25-253/Domain: trypsin homology <TRY>
F;25-111/Product: tissue kallikrein Pl light chain #status experimental <MATI>
F;112-261/Product: tissue kallikrein Pl heavy chain #status experimental <MATI>
F;65,120,213/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F. FEBS Lett. 265, 137-140, 1990
R;Title: Substrate specificity of two kallikrein family gene products isolated A;Reference number: S10698; MUID:90306305
A;Accession: S10700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-261 <BRA>
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A;Accession: A34079
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Percent Similarity:
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                                                                                                                                                                                                                                                                  160 CAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCCTCTCCGTACGGCACCC
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                                                                                                                                                                                                                                                                                                                                            67 yrSerValAsnTyrGlnValTrpLeuGlyArgAsnAsnLeuLeuGluAsp
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                             .....GCTAACGACCTCATGCTCATGCAAGTTGGACGAATCCGTGTCCGAG 276
spTyrSerAsnAspLeuMetLeuLeuHisLeuLysThrProAlaAspIle 13;
                                                                                                             oGlyPheAsnLeuAspIleIleLysAsnHisThrArgLysProGlyAsnA 116
                                                                                                                                                                                                                                 ...GluProPheAlaGlnHisArgLeuValSerGlnSerPheProHisPr
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2.846
63.095
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Gaps: 5
Percent Identity: 38.492
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seq_documentation_block:

trypsin (EC 3.4 21.4) precursor, cationic - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Mar-1998

C;Accession: A27547

R;Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.

Biochemistry 26, 3081-3086, 1987

A;Title: Isolation and characterization of a cDNA encoding rat cationic trypsinos
A;Reference number: A27547; MUID:87271609

A;Accession: A27547; MUID:87271609

A;Accession: A27547; MUID:87271609

A;Accession: A27547; MUID:9206498; PID:9206499

C;Superfamily: trypsin homology

C;Superfamily: trypsin; trypsin homology

C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;35-240/Domain: trypsin homology <TRY>
F;31-161,49-65,133-234,140-2307,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
alignment_block:
US-09-030-606-173 x A27547
                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:A27547
                                                                     Ratio:
Percent Similarity:
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Align seg 1/1

to: A27547

from: 1

6 247

seq_documentation_block:
tlssue Kallikrein (BC 3.4.21.35) mGK-22 precursor - mouse
N;Alternate names: epidezmal growth factor-binding protein typ
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1989 #sequence_revision 30-Jun-1989 #text_chang
C;Date: 08-Mar-1989 #sequence_revision 30-Jun-1989 #text_chang
C;Accession: A29746; I70039; I70038
R;Drinkwater, C.C.; Evans, B.A.; Richards, R.I.
Blochemistry 26, 670-6756, 1987
A;Title: Mouse glandular Kallikrein genes: identification and
A;Reference number: A90522; MUID:88107594

#text_change 01-Aug-1997

characterization

0f the protein type

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seq_name: pir2:A29746
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                                                                                                              AlaGlnLysGlyLysProGlyValTyrThrLysValCysAsnTyrValAs
                                                                                                                                       GGCCAAGTTGGCGTGCCAGGTGTCTACACCCAACCTCTGCAAATTCACTGA
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alignment_scores:
Quality:
Ratio:
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A; Residues: 17-54 <RE2>
A; Cross-references: GB:M18598; NID:g198555; PID:g198560
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase
F; 25-251/Domain: trypsin homology <TRY>
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A;Molecule type: DNA
A;Residues: 1-259 <br/>
A;Experimental source: strain BALB/c, salivary gland
A;Experimental source: strain BALB/c, salivary gland
A;Note: the authors translated the codon GAC for residue 210 a
A;Note: the authors translated; R. I.
J. Biol. Chem. 262, 8027-8034, 1987
A;Title: Mouse glandular kallikroin genes: Structure and part
A;Reference number: 155260; MUID:87250386
A;Accession: 170039
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecular translated from GB/EMBL/DDBJ
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A; Residues: 70-120 < RES>
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CAGAGCTCTGCGTCCCAGGC....AGAATGCCTACCGTGCTGCAGTG
                                                                                                                                                                      TIGCCTCGTTTCTGGCTGGGGTCTGCTGGCGAACGGTGAGCTCACGGGTG 382:||||||:::||||||||
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                                                                                               TGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGCTGACC 432
                                                                                                                                        rCysLeuAlaSerGlyTrpGly......
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A:Molecule type: mRNA
A:Rosidues: 127-202, "C; /204-261 <HOW>
A:Residues: 127-202, "C; /204-261
A:Cross-references: GB:X00472; NID:g54260; PID:g54261
A:Experimental source: inbred strain DBA/2J
R:Thomas, K.A.; Baglan, N.C.; Bradshaw, R.A.
J. Biol. Chem. 256, 9156-9166, 1981
A:Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S
A:Reference number: A92341; MUID:81264363
A:Accession: A92341
A;Introns: 16/1; 69/2; 165/1; 210/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; growth factor; hydrolase; serine proteinase;
F;1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                  A; Map position: 7
A; Introns: 16/1; (
                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 25-107,112-261 <THO>
A;Residues: 25-107,112-261 <THO>
C;Commental source: outbred strain Swiss Webster
C;Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer compocificomment: The active form of the gamma chain occurs naturally as combinations of eit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-261 (ULL)
A; Cross-references: GB:X01389; NID:g53373; PID:g53374
A; Cross-references: GB:X01389; NID:g53373; PID:g53374
R; HowLes, P.N.; Dickinson, D.P.; Dicaprio, L.L.; Woodworth-Gutai, M.; Gross, K.W. Nucleic Acids Res. 12, 2791-2805, 1994
A; Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth fa A; Reference number: A93510; MUID:84189573
A; Accession: A93510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; MoLecule type: DNA A; Residues: 1-261 <EVA> A; Residues: 1-261 <EVA> R; Ullrich, A; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H. R; Ullrich, B; Gray, B; Wood, W.I.; Hayflick, J.; Seeburg, P.H. DNA 3, 387-392, 1984 A; Title: Isolation of a cDNA clone coding for the gamma-subunit A; Reference number: A90949; MUID:85076169 A; Accession: A90949; MUID:85076169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 17-May-1985 #text_change 20-Mar-1998
C;Accession: A91005; A90949; A93510; A92341; A00942; A21093; A22705
R;Evans, B.A.; Richards, R.I.
EMBO J. 4, 133-138, 1985
A;Title: Genes for the alpha and gamma subunits of mouse nerve growth facto: A;Reference number: A91005; MUID:85257431
A;Accession: A91005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir1:NGMSG
                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7S nerve growth factor gamma chain (EC 3.4.21.-) precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 sValSerIleLysLeuHisProAsnGluValCysValLysAlaHisIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              476 CGTGAACGTGTCGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTC 728
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submandibular

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F:25-253/Domain: trypsin homology <TRY>
F:25-107/Domain: segment B1 <GBI>
F:25-107/Il-2-61/Product: nerve growth factor gamma chain (active form) #status experime F:112-261/Domain: segment A <GAA>
F:112-164/Domain: segment C <GCC>
F:165-261/Domain: segment B2 <GB2>
F:315-735,05-65,132-219,184-198,209-234/Disulfide bonds: #status predicted F:31-173,50-65,132-219,184-198,209-234/Disulfide bonds: #status experimental F:102/Binding site: carbohydrate (Asn) (covalent) #status experimental
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US-09-030-606-173 x NGMSG
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Quality:
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frageThrValLysProIleThrLeuProThrGluGluProLysLeuGl
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                                        GGCGGAGGGCAAGACCAGAAGGACTCCTGCAACGGTGACTCTGGGGGGGCC 604
                                                                                spCysAlaLysAlaHisIleGluLysValThrAspAlaMetLeuCysAla
                                                                                                                         TCTGCAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCC
                                                                                                                                                                 nPheThrAspAspLeuTyrCysValAsnLeuLysLeuLeuProAsnGluA
                                                                                                                                                                                                                                                                                      CTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCGTG..... 467
                                                                                                                                                                                                                                                                                                                            CGGGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGG 426
                                                                                                                                                                                                                                                                                                                                                                                                         GAACTCTTGCCTCGTTTCTGGCTGGGGGTCTGCTGGCGAACGGTGAGCTCA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spTyrSerAsnAspLeuMetLeuLeuArgLeuSerLysProAlaAspIle 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ....GCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAG 276
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2.830
61.628
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trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken N. Alternate names: trypsinogen II C; Species: Gallus gallus (chicken) C; Species: Gallus gallus (chicken) C; Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 08-Sep-1997 C; Accession: S55066; S72347 R; Wang, K.; Gan, L.; Lee, I.; Hood, L. Biochem. J. 307, 471-479, 1995 A; Tile: Isolation and characterization of the chicken trypsinogen gene family. A; Reference number: S55065 A; Accession: S75065 A; Accession: Accessio
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A,Experimental source: clone 2-P29
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine |
F:1-16/Domain: signal sequence #status predicted <SIG>F:1-25/Domain: activation peptide #status predicted <APT>F:26-248/Product: trypsin II #status predicted <APT>F:26-241/Domain: trypsin homology <TRY>F:26-241/Domain: trypsin homology <TRY>F:65,109,202/Active site: His, Asp, Ser #status predicted
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US-09-030-606-173 x S55066
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Quality:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                          160 CAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCC
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                                                                                          210 AGAGTACAACAGACCCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 TCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGAC 159
                                                                                                                                                                                          83 GlnGluAspSerGluValValArgSerSerSerValIleIleArgHisPr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 yrLysSerArgIleGlnValArgLeuGlyGluTyrAsnIleAspVal... 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 CACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTG
oLysTyrSerSerIleThrLeuAsnAsnAspIleMetLeuIleLysLeuA 116
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2.795
66.255
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Align seg 1/1

to: A29586

from: 1

6 261

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seq_documentation_block:
tissue kallikrein (EC 3.4.21.35) hGK-1 precursor - human
N;Alternate names: glandular kallikrein
C;Species: Homo sapiens (man)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 20-Mar-1998
C;Accession: A29586
R;Schedlich, L.J.; Bennetts, B.H.; Morris, B.J.
                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-261 <SCH>
A;Cross-references: GB:M18157; NID:g186640; PID:g386842
A;Note: the authors translated the codon TAC for residue
                                                                                                                                                                                                                                                                                                                                                                             A;Title: Primary structure of a human glandular kallikrein A;Reference number: A29586; MUID:88054467 A;Accession: A29586
alignment_block:
US-09-030-606-173 x A29586
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                                                                                                                   alignment_scores
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                                                           Percent Similarity:
                                                                                                                                                                           Superfamily: trypsin; trypsin homology; Keywords: hydrolase; serine proteinase; 25-253/Domain: trypsin homology CTRY>; 55,120,213/Active site: His, Asp, Ser
                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                       chedlich, L.J.; Bennetts, B.H.; Morris, B.J. 6, 429-437, 1987
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|AspTrpIleGlnGluThrIleAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysGlnGluAlaTyrProGlyAspIleThrSerAsnMetIleCysValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGG 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yrProGluLeuLeuGlnCysLeuAsnAlaProIleLeuSerAspGlnGlu 172
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                                                                                                 Quality:
                                                         449.50
2.863
61.811
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                                                         Gaps:
Identity:
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seq_documentation_block:
tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular -
tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular;
N;Alternate names: glandular prokallikrein 7, submandibular;
C;Species: Rattus norvegicus (Norway rat)
C;Species: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_chance
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                                     proteinase
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#text_change 20-Mar-1998

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A: Molecule type: mRNA
A: Residues: 43-45,'9', 47-114,'A',116-261 <BRA>
A: Residues: 43-45,'9', 47-114,'A',116-261 <BRA>
C: Superfamily: trypsin: trypsin homology
C: Keywords: hydrolase; serine proteinase
E: J1-18/Domain: signal sequence #status predicted <SIG>
F: J2-261/Product: tissue prokallikrein 7, submandibular #status
F: 25-253/Domain: trypsin homology <TRY>
F: 65,120,213/Active site: His, Asp, Ser #status predicted
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A; Residues: 25-34, D', 36-45, 'S', 47-67, 'X', 69-75 < RA2>
R; Brady, J. M.; MacDonald, R. J.
Arch. Biochem. Blophys. 278, 342-349, 1990
A; Title: The expression of two kallikrein gene family A; Reference number: $09315; MUID: 90225801
A; Accession: $09315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein A;Residues: 112-139 <EL2>
A;Residues: 112-139 <EL2>
R;Rato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Blochem. 102, 1389-1404, 1987
J. Blochem. 102, 1389-1404, 1987
A;Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi A;Reference number: A41429; MUID:88198057
A;Accession: D41429
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R;Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 112-133 < KAT> A; Accession: B41429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Molecular cloning and characterization of two rat renal kallikrein A;Reference number: A31136; MUID:89088074
A;Accession: A31136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: S10698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M19647; GB:J02837; NID:g204999; PID:g205000 R;Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F. FEBS Lett. 265, 137-140, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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A; Residues: 1-261 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: A31136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-030-606-173 x A31136
                                                                                                                                                                                                                                   110 TCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGAC
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                                                        84
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                                                                                                                                                                                                                                                                                                                                                       CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT 109
                                                                                                              CAAGAGCCAGGGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCC
                                                                                                                                                                                                                                                                                           AsnSerGlnProTrpGlnValAlaLeuTyrSerPheThrLysTyrLeuCy
AGAGTACAACAGACCCTTGCTC
                                                                                                                                                                          erSerAsnAsnTyrGlnValTrpLeuGlyArgAsnAsnLeuLeuGluAsp
                                                        ...GluProPheAlaGlnHisArgLeuValSerGlnSerPheProHisPr
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Ratio:
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2.738
64.314
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Gaps:
Percent Identity:
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A:Molecule type: mRNA
A:Residues: 1-261 <HOS>
A;Cross-references: DDB:AB016032
C;Superfamily: trypsin; trypsin homology
C;Keywords: 91ycoprotein; hydrolase; serine proteinase
F;65,120,213/Active site: His, Asp, Ser #status predicted
F;102/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                  A;Title: Expression of an allozyme of prorenin-converting enzyme A;Reference number: JE0236; MUID:98351995
A;Accession: JE0236
                                                                                                                                                                                                                                                                     C;Accession: JE0236

R;HOSO1, K.; Tadd, J.; Tsumura, K.; Kanamori, N.; Yamanaka, N.
J. Blochem. 124, 368-376, 1998
                                                                                                                                                                                                                                                                                                                                                               tissue kallikrein (EC 3.4.21.35) - mouse
N;Alternate names: prorenin-converting enzyme
C;Species: Mus musculus (house mouse)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:JE0236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 LysGluValMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             717 GAGAAAACCGTCCAG 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 GlyGlyLysAspThrCysThrGlyAspSerGlyGlyProLeuLeuCysAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 spaspHisSerasnaspLeuMetLeuLeuHisLeuSerGlnProalaasp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGAACTCTTGCCTCGTTTCTGGCTGGGGTCTGCTGGCGAACGGTGAGC 373:|||::::::||||||:::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGGCGIGCCAGGIGTCTACACCAACCICTGCAAATTCACIGAGIGGATA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCACGGGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCAGTGCGTGAACGTGTCGGTGTCTGAGGAGGTCTGCAGTAAGC 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......SerThrLysProLeuIleTrpGluPheProAspAs 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCTGACCCAGAGCTCTGCGTCCCAGGC....AGAATGCCTACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lGlySerThrCysLeuAlaSerGlyTrpGly.......
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     predicted
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                                                                                                                                                                                                                                                               in the submandibular
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alignment_scores:

Ratio: Percent Similarity:

448.50 2.786 63.889

Gaps: 6
Percent Identity: 38.492

of

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seq_documentation_block:
tissue kallikrein (EC 3.
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US-09-030-606-173 x JE0236
                                                              seq_name: pir2:S01971
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                                                                                                                                                                                                                                                                                                                                                                                                                          577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 AGAGTACAACAGACCCTTGCTC......231
                                                                                                                                                                                                                                                                                                                                     627 CAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527 GCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGACCAGAAGG 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 CAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCC 209
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83 GluGluProSerAlaGlnH1sArgLeuValSerLysSerPheProH1sPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 yrValAspGlnTyrGluValTrpLeuGlyLysAsnLysLeu...pheGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT
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  kallikrein (EC 3.4.21.35) precursor -
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                                                                                                                                                                                               ACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTG 626
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                                                                                                                                                        TC 728
                                                                                                                                                                                                                                                                                       GlnGlyThrThrSerTyrGlyProThrProCysGlyLysProGlyValPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValPheIleThrLeuLeuProAsnGluAsnCysAlaLysValTyrLeuGl 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....Thr.ProThrArgTrp., 165
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                                                                                                                                                                                                                                                                                                              426
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N;Alternate names: glandular kallikrein
(;Species: Mus musculus (house mouse)
(;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 01-Aug-1997
(;Accession: S01971; 170023
R;Drinkwater, C.C.; Richards, R.I.
Nucleic Acids Res. 16, 10918, 1988
A;Title: Sequence of mcK-11, a mouse glandular kallikrein gene.
A;Reference number: S01971; MUID:89083511
A;Accession: S01971
A;Molecule type: DNA.
A;Residues: 1-261 CDRI>
A;Cross-references: EMBL:X13215
A;Cross-references: EMBL:X13215
A;Cross-references: EMBL:X13215
A;Cross-references: EMBL:X13215
A;Cross-references: EMBL:X13215
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(;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>F;18-24/Domain: propeptide #status predicted <PRO>F;25-261/Product: tissue kallikrein #status predicted <MAT>F;25-253/Domain: trypsin homology <TRY>F;65,120,213/Active site: His, Asp, Ser #status predicted
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J. Biol. Chem. 262, 8027-8034, 1987
A;Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis A;Reference number: I55260; MUID:87250386
A;Accession: I70023
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 70-122 <RES>
A;Cross-references: GB:M18610; NID:g198529; PID:g198537
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
Quality:
Ratio:
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133 ThrAspAlaValLysProIleAlaLeuProThrGluGluProLysLeuGl 149
                                                                                                                                                                                        277 TCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGG
                                                                                                                                                                                                                                                       116 spGluSerAsnAspLeuMetLeuLeuArgLeuSerGluProAlaAspIle 132
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Sequence Strid Orig 52 Score Escore Len | Documentation |
SvissProt_37 SCCE_HUMAN | 5.50.50 | 500.54 | 100-20 | 244 | P36575 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.50.00 | 441.90 | 1.90-17 | 259 | P36376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.50.00 | 431.95 | 1.90-17 | 259 | P36376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.50.00 | 431.95 | 1.90-17 | 259 | P36376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.50.00 | 431.95 | 4.90-17 | 259 | P36376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.50.00 | 431.95 | 4.90-17 | 259 | P36376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.00 | 431.95 | 4.90-17 | 261 | P306376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.00 | 431.95 | 4.90-17 | 261 | P306376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.95 | 4.90-17 | 261 | P306376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.95 | 4.90-17 | 261 | P306376 rattus norvegicus (rat) |
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SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.95 | 5.20-17 | 261 | P306376 rattus norvegicus (rat) |
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SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.95 | 5.20-17 | 261 | P306376 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.95 | 5.20-17 | 261 | P306476 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.95 | 5.20-17 | 261 | P306476 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.50 | 431.70 | 6.60-17 | 261 | P306476 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.50 | 431.70 | 6.60-17 | 261 | P306476 rattus norvegicus (rat) |
SvissProt_37 SCCE_HUMAN | 4.40.50 | 431.95 | 431.90 | 431.95 | 431.90 | 431.95 | 431.90 | 431.95 | 431.90 | 431.95 | 431.90 | 431.95 | 431.90 | 431.95 | 431.90 | 431.95 | 4
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-MODEL-frame+n2p.model -DEV-xlp
-Q-/Ggn2_1/USPT0_spool_VIS09030606/runat_24091999_171618_29883/app_query.fasta.1
-DB-SwissProt_37 -QFMT-fastan -SUFFIX=rsp -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPELT-0.000 -LOOPEXT-0.000
-GAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-FGAPOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-escore
-ALIGN-15 -MODE-LOCAL -OUTFMT-PF6 -NORM-stat -USER-US09030606
-NCPU-6 -ICPU-3 -WAIT -THREADS-1
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Query: US-09-030-606-173
Query length: 1265
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Database sequences: 77977
Database length: 28268293
Search time (sec): 155.430000
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         SwissProt_37:KLK4_MOUSE
SwissProt_37:ESTA_CANFA
SwissProt_37:TRY2_CANFA
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Primary Substrate specificity of recombinant human stratum corneum RT "Primary Substrate specificity of recombinant human stratum corneum RT chymotryptic enzyme.";

RL BIOCHEM. BIOPHYS. RES. COMMUN. 211:586-589(1995).

CC -!- FUNCTION: MAY CATALYZE THE DEGRADATION OF INTERCELLULAR COHESIVE STRUCTURES IN THE CONNIFIED LAYER OF THE SKIN IN THE CONTINUOUS CONSIDERS WITH AROMATIC SIDE CHAINS IN THE PROSITION. SCCE CLEAVES INSULIN B CHAIN AT 6-LEU-1-CYS-7, 16-TYR-1-LEU-17, 25-PHE-1-TYR-25, AND 26-TYR-1-THR-27. COULD PLAY A ROLE IN THE ACTIVATION OF PRECURSORS TO INFLAMMATORY CYTOKINES.

-!- TISSUE SPECIFICITY: IT IS ABUNDANTLY EXPRESSED BY KERATINOCYTES IN THE EPIDERMIS. VERY LOW LEVELS ARE ALSO SEEN IN THE BRAIN AND KIDNEY.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: SwissProt_37:SCCE_HUMAN
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01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER; PF00139; trypsin; 1. HSSP; P00763; 1DP0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HANSSON L., STROEMQVIST M., BAECKMAN A., WALLBRANDT P., CARLSTEIN
EGELRUD T.;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Experiment of the Experim
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ACTIVATION PEPTIDE.
STRATUM CORREGUM CHYMOTRYPTIC ENZYME.
STRATUM CORREGUM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
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                                  CCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAG
                                                                          TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGl
                                                                                                               TTCGGAAAAGCCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAA 691
                                                                                                                                                      spSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer
                                                                                                                                                                          ACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCT
                                                                                                                                                                                                                                  rMetLeuCysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyA
                                                                                                                                                                                                                                                                           CATGTTCTGCGCCGGCGGAGGGCCAAGACCAGAAGGACTCCTGCAACGGTG
                                                                                                                                                                                                                                                                                                                  IleSerProGlnAspCysThrLysValTyrLysAspLeuLeuGluAsnSe
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nValCysLysPheThrLysTrpIleAsnAspThrMetLys
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seq_name:

SwissProt_37:KLKA_RAT

EMBL; S48142; G259431; -. PIR; A35545; A35545.

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Seq_documentation_block:
ID KKAA_RAT STANDA
AC 936775;
DT 01-JUN-1994 (REL. 29,
DT 01-JUN-1994 (REL. 29,
DT 01-WN-1997 (REL. 35,
DE GLANDULAR KALLIKREIN
(REC. 29,
DT 01-WOY-1997 (REL. 35,
DE GLANDULAR KALLIKREIN
(REC. 35,
DE GLANDULAR KALLIKREIN
(REC. 35,
DE GLANDULAR KALLIKREIN
(REC. 36,
OC ROTENTA, METAZOA;
CC RODENTIA, SCIUROGNATH
RN (1)
RC TISSUE-SUBMANDIBULAR
RN MEDLINE; 93041794.
RN MA J.-X., CHAO J., CH
RT "MOLECULAR Cloning at
RT MININGENASE from rat
RT KININGGENASE from rat
RT KININGGENASE from rat
RT MININGGENASE from rat
RT "MOLECULES OF 10-32 AN
RT SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                  KATO H., MARANISHI E., ENJYOJI K., HAYASHI I., OH-ISHI S., IWANAGA "Characterization of serine proteinases isolated from rat submaxillary gland: with special reference to the degradation of ra kininogens by these enzymes.";
J. BICCHEM. 102:1389-1404(1987).
-1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 91224135.
GUTMAN N., ELMOUJAHED A., BRILLARD M., DU SORBIER B., GAUTHIER F.;
"Microheterogeneity of rat submaxillary gland kallikrein k10, a
member of the kallikrein family.";
EUR. J. BIOCHEM. 197:425-429(1991).
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01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-JUN-1997 (REL. 25, LAST ANNOTATION UPDATE)
GLANDULAR KALLIKREIN 10 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN)
(T-KININOGENASE) (K10) (PROTEINASE B) (ENDOPEPTIDASE K) (FRAGMENT).
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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EUKARYOTA; METAZOA; CHORDATA; VEI
RODENTIA; SCIUROGNATHI; MURIDAE;
                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and characterization of rKlk10, a cDNA encoding kininogenase from rat submandibular gland and kidney."; BIOCHEMISTRY 31:10922-10928(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 10-32 AND 97-117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Purification and characterization of T-kininogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 10-32 AND 97-133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XIONG W., CHEN L.-M., CHAO J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISSUE-SUBMAXILLARY GLAND;
                                                                                                                                                                                                                                                                                                                TRYPSIN FAMILY. BELONGS TO THE GLANDULAR KALLIKREIN SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHEM. 265:2822-2827(1990).
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91224135.
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PIR; A44284; A44284.
PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
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GGGGAACTCTTGCCTCGTTTCTGGCTGGGGGTCTGCTGGCGAACGGTGAGC
                                                                     GAGTCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGC 323
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                                 IleThrAspGlyValLysValIleAspLeuProThrGluGluProLysVa
                                                                                                                 spAspTyrSerAsnAspLeuMetLeuLeuHisLeuSerGluProAlaAsp 114
                                                                                                                                                                                                 oAspTyr...LysProPheLeuMetArgAsnH1sThrArgGlnArgGlyA
                                                                                                                                      ......GCTAACGACCTCATGCTCATGCAGTTGGACGAATCCGTGTCC 273
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T-KININOGENASE LIGHT CHAIN.
T-KININOGENASE HEAVY CHAIN
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ACTIVATION PEPTIDE (PROBABLE).
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CARNIVORA;
[1]
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com entities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                             PINSKY S.D., LAFORGE K.S., SCHEELE G.;

"Differential regulation of trypsinogen mRNA translation: full-length mRNA sequences encoding two oppositely charged trypsinogen isoenzymes in the dog pancreas.",

MOL. CELL. BIOL. 5:2669-2676(1985).

-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.

-!- SUBCELLULAR LOCATION: EXTRACELLULAR.

-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
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01-JAN-1988 (REL. 06, LAST SEQUENCE UF
01-NOV-1995 (REL. 32, LAST ANNOTATION
TRYPSINGEN, CATIONIC PRECURSOR (EC 3.
CANIS FAMILIARIS (DOG).
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                                                            EMBL; M11590; G164097; -. PIR; B26273; TRDGC.
                                                                                                         or send an email to license@isb-sib.ch).
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FISSIPEDIA;
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PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER; PFAM; PF000899; trypsin; 1. HSSP; P00761; 1EPT.

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alignment_block:
US-09-030-606-173 x TRY1_CANFA
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Quality:
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                                                                                                                                      GGTCCTCTGCCCAGTCGCGGGGGGCTGACCCAGAGCTCTGCGTCCCAGGCA
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                      ValCysArgAsnAlaTyrProGlyGlnIleSerSerAsnMetMetCysLe
                                                                   snTyrProAspValLeuGlnCysLeuLysAlaProIleLeuSerAspSer
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                                                                                                                                                                                                                                     AGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCCGCACTCGCAGCCCTGGCAGGCGCACTGGTCATGGAAAACGAATT
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                                                                                                                 ysLeuSerSerProAlaThrLeuAsnSerArgValSerAlaIleAlaLeu
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLANDULAR KALLIKREIN 12, SUBMANDIBULAR/RENAL PRECURSOR (EC 3.4.21.35)
                                                                                                                                                                                                                                EMBL; M19648; G205004; -.
EMBL; M22922; G205004; JOINED.
PIR; B31136; B31136.
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CHEN Y.-P., CHAO J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235
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                                                                                                                                 SIGNAL
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HSSP; P00759; 1TON.
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KLK12 OR KLK-12.
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                                                                                                                                               MULTIGENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                 KALLIDIN (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS MET-|-XAA OR LEU-|-XAA THE SECTIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. BELONGS TO THE GLANDULAR KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
IN KININOGEN TO RELEASE LYS-BRADYKINUK CLEAVAGE OF ARG-1-XAA BONDS IN
CATALYTIC ACTIVLTY: PREFERENTIAL CLEAVAGE OF ARG-1-XAA BONDS IN
SMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE
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                                                                                                                                              ZYMOGEN;
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alignment_block:
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CARBOHYD
SEQUENCE
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                                            GTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTG
                                                                                                                CAGAAGGACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGG 619
                                                                                                                                                                                                     GCAGTGCGTGAACGTGTCGGTGGTGTCTGAGGAGGTCTGCAGTAAGCTCT 519
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                                                                                                                                                                                                                                                                                                                                                                                   ySerThrCysLeuAlaSerGlyTrp...........
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                           yValLeuGlnGlyIleThrSerTrpSerSerValProCysGlyGluThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ....GCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAG 276
                                                                                                                                             isThrGlnMetValThrAspValMetLeuCysAlaGlyGluLeuGluGly
                                                                                                                                                                         ATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGAC 569
                                                                                                                                                                                                                                                               .....SerSerThrLysProLeuGluTrpGluPheProAspAspLe
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91
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2.758
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91
106
28759
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POTENTIAL.

POTENTIAL.

Od4C9EF5 CRC32;
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                             236
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seq_documentation_block:
ID KLK8_RAT STANDARD;
alignment_scores:
Quality:
                                                           seq_name: SwissProt_37:KLK8_RAT
                                                                                                                                                                                                                                                                                                      EMBL; M27217; G206640; JOINED.
EMBL; M27215; G206640; JOINED.
EMBL; M27216; G206640; JOINED.
PIR; A34079; A34079
PROSITE; PS00134; TRYPSIN_HIS; 1
PROSITE; PS00135; TRYPSIN_SER; 1
                                                                       DISULFID
CARBOHYD
                                                                                                  ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLK8 OR KLA-6.
RATTUS NORVEGICUS (RAT).
REUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUKARYOTA; METAZOATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLANDULAR KALLIKREIN 8, PROSTATIC PRECURSOR (EC KALLIKREIN) (PI KALLIKREIN) (RGK-8).
KLK8 OR KLK-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 89352606.
BRADY J.M., WINES D.R., MACDONALD R.J.;
"Expression of two kallikrein gene family members in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate.";
BIOCHEMISTRY 28:5203-5210(1989)
                                                                                                                                                                                                                                                                              PFAM; PF00089; trypsin; 1. HSSP; P00759; ITON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                 HYDROLASE; SERINE PROTEASE; KININOGENASE; GLYCOPROTEIN;
MULTIGENE FAMILY; ZYMOGEN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS IN KININOGEN TO RELEASE LYS-BRADYKININ.
CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-|-XAA BONDS IN SMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluValMetLys 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KALLIDIN (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS MET-|-XAA OR LEU-|-XAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYPSIN FAMILY. BELONGS TO THE GLANDULAR KALLIKREIN SUBFAMILY.
                                                                                        19
65
120
120
213
31
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152
184
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                                                         29013
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                                                                    CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                                                                                                                      ACTIVATION PEPTIDE (PROBABLE) GLANDULAR KALLIKREIN 8.
                                                                                                                                                                                                                                     PROBABLE
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                                                         AE5E2FF1 CRC32;
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RATTUS.
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Ratio:

452.50 2.846

Length: Gaps:

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alignment_block:
US-09-030-606-173 x KLK8_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 TCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spTyrSerAsnAspLeuMetLeuLeuH1sLeuLysThrProAlaAspIle 132
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                                     TCCAG
                                                                    oSerValTyrThrLysLeuIleLysPheThrSerTrpMetLysLysValM
                                                                                                                                         GlnGlyIleThrSerTrpGlySerMetProCysGlyGluProAsnLysPr
                                                                                                                                                                            CAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCC
                                                                                                                                                                                                                splleCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyValLeu
                                                                                                                                                                                                                                                   ACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTG
                                                                                                                                                                                                                                                                                 pGluValThrAspValMetLeuCysAlaGlyGluMetAspGlyGlyLysA
                                                                                                                                                                                                                                                                                                                        GCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGG
                                                                                                                                                                                                                                                                                                                                                           ValAsnIleHisLeuLeuSerAsnGluLysCysIleLysAlaTyrAsnAs 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCTGCAGTGC 476
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etLys
                                                                                              AGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....Pro..LeuLys......
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   258
                                     731
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seq_name: SwissProt_37:TRY3_RAT

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Seq_documentation_block:
ID TRY3_RAT STANDA
AC PO8426;
DT 01-AUG-1988 (REL. 08,
DT 01-AUG-1988 (RELOR 08,
D
                                                                                                                                                                                                                                                                       alignment_block:
US-09-030-606-173 x TRY3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                     Align seg 1/1 to: TRY3_RAT
                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A27547; A27547
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
PF00089; Trypsin; 1.
HSSP; P00763; 1DP0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    III).
RATTUS NORVEGICUS (RAT).
RHTARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RHKARYOTA; METAZOA; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P08426;
01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TRYPSINOGEN III, CATIONIC PRECURSOR (EC 3.4.21.4) (PRETRYPSINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypsinogen.";
BIOCHEMISTRY 26:3081-3086(1987).
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-1- SUBCELLULAR LOCATION: EXTRACELLULAR.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIETCHER T.S., ALHADEFF M., CRA: "Isolation and characterization
     49
                                                          60
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                                                                                                                                                                     10
AsnSerLeuProTyrGlnValSerLeu...AsnAlaGlyTyrHisPheCy
                                                                                                                                                               CACTCGCAGCCCTGGCAGGCGCACTGGTCATGGAAAACGAATTGTTCTG
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68.313
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                         Percent
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tion of a cD
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Identity:
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RATTUS.
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seq_name:
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                                                                                                                                          P15948;
01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GLANDULAR KALLIKREIN K22 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN)
(MEK-22) (EPIDERMAL GROWTH FACTOR-BINDING PROTEIN TYPE A) (EGF-BP A)
(NERVE GROWTH FACTOR BETA CHAIN ENDOPEPTIDASE) (BETA-NGF-
STRAIN-BALB/C; TIS
MEDLINE; 88107594.
DRINKWATER C.C., F
                                                                         KLK22 OR KLK-22.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VEI
RODENTIA; SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560
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                                               SEQUENCE FROM
                                                                                                                                        ENDOPEPTIDASE)
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                                 TISSUE-SALIVARY GLAND
                                                                                                                                                                                                                                                               STANDARD;
   EVANS B.A.,
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   RICHARDS
                                                                            VERTEBRATA; MAMMALIA; AE; MURINAE; MUS.
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                          247
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   R. I.;
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                                                                                            EUTHERIA;
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EMBL; M17979; G387167; ALT_SEO.

EMBL; M17977; G387167; JOINED.

EMBL; M1978; G387167; JOINED.

EMBL; M18598; G198560; -.

EMBL; M18618; G198561; -.

PIR; A29746; A29746.

PIR; A38356; A38356.
           CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                        PIR; A383
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. BIOL. CHEM. 262:8027-8034 (1987).

-I- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONI IN KININOGEN TO RELEASE LYS-BRADYKININ.

-I- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-|-XAA BONDS IISMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE KALLIDIN (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS MET-|-XAA OR LEU-|-XAA.

-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1: ALSO KNOWN AS THE TRYPSIN FAMILY. BELONGS TO THE GLANDULAR KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETERS J., TAKAHASHI S., TADA M., MIYAKE Y.;
"mGK-6-derived true tissue kallikrein is synthesized,
targeted through a regulated secretory pathway in mous
AtT-20 cells.";
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mouse glandular kallikrein genes. Structure and partial sequence analysis of the kallikrein gene locus.";
J. BIOL. CHEM. 262:8027-8034(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 91190897.
FAHNESTOCK M., WOO J.E.,
MOBLEY W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mouse glandular kallikrein genes: characterization of the genes encod binding proteins.";
BIOCHEMISTRY 26:6750-6756(1987).
                                                                                                                                                                                                PFAM; PF00089; trypsin; HSSP; P00757; 1SGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Beta-NGF-endopeptidase: encoded by the gene mGK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 25-54.
MEDLINE; 91190897.
                                                                                                                                                            SIGNAL
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                                                                                                                                            PROPEP
                                                                                                                                                                       MULTIGENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . BIOCHEM. 111:643-648(1992).
                                                                                                                                                                                                                          PS00134; TRYPSIN_HIS; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87250386
                                                                                                                                                                       FAMILY;
                                                                                                                                                                                  SERINE PROTEASE;
                       18
25
65
118
118
211
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182
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                                                                                                                                                                     ZYMOGEN;
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                                                                                                                                                                     KININOGENASE; GLYCOPROTEIN; SIGNAL.
                    GLANDULAR KALLIKREIN K
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                                                            ACTIVATION PEPTIDE
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3B02165A CRC32;
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                                                                                                         GCAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGC
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                          GTC 728
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                                                                                                                                                                                                                                                                             sValSerIleLysLeuHisProAsnGluValCysValLysAlaHisIleL 188
                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGGCTGACC
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SEQ_documentation_block:
ID KIK3_MOUSE STANNA
AC PO0756:
DT 121-JUL-1986 (REL. 01,
DT 21-JUL-1988 (REL. 36,
DE GLANDULAR KALLIKREIN
DE (MGK-3) (75 NERVE GRO
GN KIK3 OR KIK-3 OR NOFG
GN KIK3 OR NOFG
GN KIK3 OR KIK-3 OR NOFG
GN KIK3 OR NOFG
GN KIK-3 OR NOFG
GN KIK3 OR KIK-3 OR NOFG
GN KIK-3 OR NOFG
GN KIK3 OR OR 
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EMBL; X01389; G53374; -.
EMBL; X01798; G582429; -.
EMBL; X01799; E73575; -.
PIR; A00942; MGMGG.
PDB; 1SGF; 27-MAY-98.
MGD; MGI:97322; NGFG.
PROSITE; PS00134; TRYPSIN_i
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21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GLANDULAR KALLIKREIN K3 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN)
(MGK-3) (75 NERVE GROWTH FACTOR GAMMA CHAIN) (GAMMA-NGF).
KLK3 OR KLK-3 OR NGFG.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of mouse 75 NGF: a complex of nerve growth factor with four binding proteins.";
STRUCTURE 5:1275-1285(1997).
-I- FUNCTION: 75 NGF ALPHA CHAIN STABILIZES THE 75 COMPLEX. THE BE DIMER PROMOTES NEURITE GROWTH. THE GAMMA CHAIN IS AN ARGININE-SPECIFIC PROTEASE; IT MAY ALSO HAVE PLASMINGEN ACTIVATOR ACTIVITY, AS WELL AS MITOGENIC ACTIVITY FOR CHICK EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "THOMAS K.A., BAGLAN N.C., BRADSHAW R.A.;
"The amino acid sequence of the gamma-subunit gland 7 S nerve growth factor.";
J. BIOL. CHEM. 256:9156-9166(1981).
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"Genes for the alpha and
are contiguous.";
EMBO J. 4:133-138(1985).
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BAX B., BLUNDELL T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ULLRICH A., GRAY A., WOOD W.I., HAYFLICK J., SEEBURG P.H.; "Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth factor using a high-stringency selection procedure."; DNA 3:387-392(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: 75 NERVE GROWTH FACTOR IS COMPOSED OF TWO ALPHA CHAINS, A BETA DIMER COMPOSED OF IENTICAL CHAINS, AND TWO GAMMA CHAINS. THIS PRECURSOR IS CLEAVED INTO SEGMENTS TO PRODUCE THE ACTIVE FORM OF THE GAMMA CHAIN, WHICH OCCURS NATURALLY AS COMBINATIONS OF EITHER TWO OR THREE SEGMENTS HELD TOGETHER BY DISULFIDE BONDS: B1 + A OR B1 + C + B2.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN FAMILY. BELONGS TO THE GLANDULAR KALLIKREIN SUBFAMILY.
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TRYPSIN_HIS;

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alignment_block:
US-09-030-606-173 x KLK3_MOUSE
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ACT_SITE
ACT_SITE
DISULFID
DISULFID
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SEQUENCE
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DOMAIN
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SIGNAL
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PFAM; PF00089; LTYPS11; 1.
HYDROLASE; SERINE PROTERSE; KININGENASE; GLYCOPROTEIN;
MULTIGENE FAMILY; ZYMOGEN; SIGNAL; GROWTH FACTOR; 3D-ST
                                                                         149
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                                                                       ySerThrCysLeuAlaSerGlyTrpGlySerIleThr......
                                                                                                 GAACTCTTGCCTCGTTTCTGGCTGGGGGTCTGCTGGCGAACGGTGAGCTCA 376
                                                                                                                         ThrAspThrValLysProIleThrLeuProThrGluGluProLysLeuGl
                                                                                                                                                 TCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGG
                                                                                                                                                                          spTyrSerAsnAspLeuMetLeuLeuArgLeuSerLysProAlaAspIle 132
                                                                                                                                                                                                   .....GCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAG
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                                                                                                                                                                                                                                                  AGAGTACAACAGACCCTTGCTC...............
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                                                                                                                                                                                                                                                                                                                                                                                                        CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT
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                                                CGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGG
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NERVE GROWTH FACTOR GAMMA C
NERVE GROWTH FACTOR GAMMA C
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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SEGMENT A.
SEGMENT B2.
SEGMENT B2.
SEGMENT B2.
7B9C5256 CRC32;
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Identity: 35
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seq_name: SwissProt_37:TRY3_CHICK
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HSSP; P00763; 11
HYDROLASE; SERII
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O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TRYPSINOGEN II-P29 PRECURSOR.
GALLUS GALLUS (CHICKEN).
GUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PHASIANINAE; GALL
SIGNAL
PROPEP
CHAIN
ACT_SITE
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95251611.
WANG K., GAN L., LEE I., HOOD L.E.;
"Isolation and characterization of the chicken trypsinogen
                                                                                                                                  EMBL; U15157; G603907; PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                BIOCHEM. J. 307:471-479(1995).
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 nPheThrAspAspLeuTyrCysValAsnLeuLysLeuLeuProAsnGluA
                                                                     MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRY3_CHICK
                                                                                                                                                                                                                                                                                                                                              LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGAGTGGATAGAGAAAACCGTC 728
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                                                                                    SERINE PROTEASE;
   17
26
65
                                                                                                                      trypsin;
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16
25
248
65
BY SIMILARITY.
ACTIVATION PEPTIDE (ITRYPSIN II-P29.
CHARGE RELAY SYSTEM
                                                                                     DIGESTION; PANCREAS;
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                                   (BY SIMILARITY).
                                                                                     ZYMOGEN; SIGNAL;
 (BY SIMILARITY)
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laSerAlaValGluTyrSerAlaAspIleGlnProIleAlaLeuProSer 132
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                              TGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCCG
                                                          yPheLeuGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProV
                                                                                       CGGAGGGCAAGACCAGAAGGACTCCTGCAACGGTGACTCTGGGGGGCCCCC
                                                                                                                  CysGlnGluAlaTyrProGlyAspIleThrSerAsnMetIleCysValGl
                                                                                                                                                TGCAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCCGG
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seq_name: SwissProt_37:KLK2_HUMAN
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                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                             "Identification and androgen-regulated expression of two major human glandular kallikrein-1 (hcK-1) mrna species.";

MOL. CELL. ENDOCRINOL. 76:181-19(1991).

-i- EUNCTION: GLANDULAR KALLIKRBINS CLEAVE MET-LYS AND ARG-SER BONDS IN KININOGEN TO RELEASE LYS-BRADYKININ.

-i- CATALTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-|-XAA BONDS IN SMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE KALLIDIN (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS OF MET-|-XAA OR LEU-|-XAA.

-i- SIMILABITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE MET-PARTY: BELONGS TO PETIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                  EMBL; M18156; -; NOT_ANNOTATED_CDS.
EMBL; M18157; G386842; -
EMBL; S39329; E79223; -
PIR; A29586; A29586.
MIM; 147960; -
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RIEGMAN P.H., VLIETSTRA R.J., DER KORPUT H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES: CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35)
                                                                                     MULTIGENE
SIGNAL
                                                                                                                           PROSITE; PS00134; TRYPS: PROSITE; PS00135; TRYPS: PFAM; PF00089; trypsin; HSSP; P07288; 1PFA.
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Primary structure of a human DNA 6:429-437(1987).
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                                                                                                                HYDROLASE;
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TRYPSIN_SER;
                                                                                                               PROTEASE;
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GLANDULAR KALLIKREIN 2
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                             KININOGENASE;
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glandular kallikrein gene.";
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GlnGlyIleThrSerTrpGlyProGluProCysAlaLeuProGluLysPr
                             CAGGGCCTTGTGTCTTTCGGAAAAGCCCCCGTGTGGCCAAGTTGGCGTGCC
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PIR; B41429; B41429

PROSITE; PS00134; TRYPSIN_HIS; 1

PROSITE; PS00135; TRYPSIN_SER; 1

PFAM; PF00089; TIYPSIN; 1

HSSP; P00759; ITON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                **RATO H., NAKANISHI E., ENJYOJI K., HAYASHI I., OH-ISHI S., IWANAGA S.

"Characterization of serine proteinases isolated from rat

submaxiliary gland: with special reference to the degradation of rat

kininogens by these enzymes.";

J. BIOCHEM. 102:1389-1404(1987).

-I- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS

IN KININOGEN TO RELEASE LYS-BRADYKININ.

-I- CATALUTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-|-XAA BONDS IN

SMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE

KALLIDIN (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS OF

KALLIDIN (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLK7_RAT
P36373;
   CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUKARYOTA; MORINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 39, LAST ANNOTATION UPDATE)
01-MOV-1997 (REL. 39, LAST ANNOTATION UPDATE)
GLANDULAR KALLIKREIN 7, SUBMANDIBULAR/RENAL PRECURSOR (EC 3.4.
(TISSUE KALLIKREIN) (RGK-7) (RSKG-7) (ESTERASE B) (PROTEINASE KLK7 OR KLK-7.
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 89088074. CHEN Y.-P., CHAO J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             677
                                                                                  SIGNAL
PROPEP
                                                                                                                                                                                                                                                    EMBL; M19647; G205000; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-SUBMAXILLARY GLAND; MEDLINE; 88198057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOCHEMISTRY 27:7189-7196(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and characterization of
                                                                                                                     MULTIGENE
                                                                                                                                      HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 25-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCG
|:::|||||||::: | ||||
oAlaValTyrThrLysValValHisTyrArgLysTrpIleLysAspThrI
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leAlaAlaAsn
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                                                                                                                     FAMILY;
                                                                                                                                  SERINE PROTEASE; KININOGENASE; GLYCOPROTEIN;
   19
25
65
120
213
31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260
                                                                                                                     ZYMOGEN;
   18
24
261
65
120
173
ACTIVATION PEPTIDE (PROBABLE).
GLANDULAR KALLIKREIN 7.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                                     SIGNAL
                                                                                                     PROBABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
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alignment_scores:
Quality:
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US-09-030-606-173 x KLK7_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: KLK7_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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DISULFID
DISULFID
DISULFID
CARBOHYD
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT 109
                            GACCAGAAGGACTCCTGCAACGGTGACTCTGGGGGGCCCCTGATCTGCAA
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GlyGlyLysaspThrCysThrGlyAspSerGlyGlyProLeuLeuCysas
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                                                                                                                       TCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAA 566
                                                                                                                                                                                GCTGCAGTGCGTGAACGTGTCGGTGGTGTCTGAGGAGGTCTGCAGTAAGC
                                                                                                                                                                                                                                                                                                           TCACGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGG 423
                                                                                         spaspHisSerasnaspLeuMetLeuLeuHisLeuSerGlnProAlaasp 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oAspTyr...LysProPheLeuMetArgAsnHisThrArgLysProGlyA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sGlyGlyValLeuIleAspProSerTrpValIleThrAlaAlaHisCysS
CGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCCGTGTGGCCAAG
                                                                                                                                                    pLeuGlnCysValAsnIleHisLeuLeuSerAsnGluLysCysIleLysA 187
                                                                                                                                                                                                                .....SerThrLysProLeuIleTrpGluPheProAspAs
                                                                                                                                                                                                                                                                                                                                        .....GCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCC
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152
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209
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2.738
64.314
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198
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BY SIMILARITY.
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BY SIMILARITY.
POTENTIAL.
S -> D (IN REF.
T -> S (IN REF.
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C -> S (IN REF. 2)
27B65B42 CRC32;
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Gaps:
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Seq_documentation_block:
ID KLKA_MOUSE CTAN
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                            EMBL; X13215; G53066; -
EMBL; X13216; G582395; ALT_SEQ.
EMBL; X13217; E14069; -
EMBL; X13217; E14070; -
EMBL; X13218; E7100; -
EMBL; X13218; E7100; -
EMBL; M18590; G554179; ALT_SEQ.
EMBL; M18590; G554179; ALT_SEQ.
EMBL; M18590; G554179; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                 PVANS B.A., DRINKWATER C.C., RICHARDS R.I.;

"Mouse glandular kallikrein genes. Structure and partial sequence analysis of the kallikrein gene locus.";

J. BIOL. CHEM. 262:8027-8034(1987).

-!- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS IN KININOGEN TO RELEASE LYS-SHADYKININ.

-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-|-XAA BONDS IN SMALL MOLECULE SUBSTRATES. HIGHLY SELECTIVE ACTION TO RELEASE KALLIDIN (LYSYL-BRADYKINI) FROM KININOGEN INVOLVES HYDROLYSIS OF KALLIDIN (LYSYL-BRADYKINI) FROM KININOGEN INVOLVES HYDROLYSIS OF MET-|-XAA OR LEU-|-XAA.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLANDULAR KALLIKREIN K11 PRECURSOR (EC 3.4.21.
(TISSUE KALLIKREIN) (MGK-11).
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVANS B.A., RICHARDS R.I.;
"Genes for the alpha and gamma subunits are contiguous.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRINKWATER C.C., RICHARDS R.I.; "Sequence of mGK-11, a mouse glandular kallikrein gene."; NUCLEIC ACIDS RES. 16:10918-10918(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLK11 OR KLK-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysGluValMetLys 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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MUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth factor
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TRYPSIN_HIS;

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alignment_block:
US-09-030-606-173 x KLKA_MOUSE
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W MULTIGENE FAMILY; ZYMOGEN; SIGNAL
T SIGNAL
T 1 18
PROBABLE.
T PROPED 19 24
ACTIVATION PEPTIDE (PROBABLE)
T CHARN
T CAT.SITE 65 65
CHARGE RELAY SYSTEM.
ACT.SITE 120 120
CHARGE RELAY SYSTEM.
T ACT.SITE 213 213
CHARGE RELAY SYSTEM.
T ACT.SITE 213 213
DISULFID 31 173
DISULFID 50 66
BY SIMILARITY.
T DISULFID 50 66
BY SIMILARITY.
T DISULFID 152 219
DISULFID 152 219
DISULFID 184
DISULFID 198
DISULFID 199
DISULFID 209
SEQUENCE 261 AA; 28727 MW; FD904C22 CRC32;
                                477
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HSSP; P00757; 1SGF.
HYDROLASE; SERINE PROTEASE
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ValSerIleLysLeuLeuProAsnGluValCysValLysAsnHisAsnGl
               GTGAACGTGTCGGTGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGACCC
                                                                                                                                                                                      GAACTCTTGCCTCGTTTCTGGCTGGGGGTCTGCTGGCGAACGGTGAGCTCA
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                                                                                                                                                          CGGGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGG
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Gaps:
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seq_name: SwissProt_37:PROS_HUMAN
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MEDLINE; 89183632.

DIGBY M.R., ZHANG X.Y., RICHARD R.I.;

DIGBY M.R., ZHANG X.Y., RICHARD R.I.;

"Human prostate specific antigen (PSA)

the kallikrein-like gene, hGK-l.";

the kallikrein-like gene, hGX-l.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROS_HUMAN
P07288;
01-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
"CDNA coding for the entire human prostate specific antigen high homologies to the human tissue kallikrein genes."; BIOCHEM. BIOPHYS. RES. COMMUN. 160:903-910(1989).
                                                                                                              TISSUE-PROSTATE;
MEDLINE; 87190978.
LUNDWALL A., LILJA H.;
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FEBS LETT. 214:317-322(1987).
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01-JUL-1989 (REL. 11, LAST SEGUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROSTATE SPECIFIC ANTIGEN PRECURSOR (EC 3.4.21.77) (PSA) (GAMMA-SEMINOPROTEIN) (SEMENOGELASE) (SEMININ) (P-30 ANTIGEN).
                                                                                                                                                                                                                                 "Characterization of the gene for prostate-specific antigen, glandular kallikrein.";
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LUNDWALL A.;
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KLOBECK H.-G.,
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
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                                                                  TISSUE-PROSTATE;
MEDLINE; 89246551
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                   BIOCHEM. BIOPHYS.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             KLOBECK H.-G., COMBRIATO G., SCHULZ P., ARBUSOW V., FITTLER "Genomic sequence of human prostate specific antigen (PSA)." NUCLEIC ACIDS RES. 17:3981-3981(1989).
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMATES; CATARRHINI; HOMINIDAE;
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SEQUENCE OF 25-261.

MEDLINE: 86205857.

MATT K.W.K., LEE P.J., M'TIMKULU T., CHAN W.P., LOOR R.;

"Human prostate-specific antigen: structural and functional similarity with serine proteases.";

similarity with serine proteases.";

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"ISOlation, characterization and amino-acid sequence of gamma-
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EMBL;
                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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"Characterization of the prostate-specific antigen gene: human kallikrein-like gene.";
BIOCHEM. BIOPHYS. RES. COMMUN. 159:95-102(1989).
                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
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MONNE M.M., MORENO J.
SUBMITTED (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence of a cDNA clone encompassing the prostate specific antigen (PSA) and an unsp. NUCLEIC ACIDS RES. 16:6226-6226(1988).
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TISSUE-PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A structural model
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L; X14810; G296671; -.
L; X13940; G35723; -.
L; X13941; E14018; ALT_SEQ.
L; X13942; E14019; -.
L; X13943; E14020; -.
L; X13944; E14022; -.
L; X05332; G35741; -.
L; X05332; G35741; -.
L; X05332; G35741; -.
L; X07300; -; NOT_ANNOTATED_
3L; M27274; G190553; -.
3L; M27274; G190553; -.
3L; M276663; G618464; -.
3L; M276663; G618464; -.
3L; M276663; G51857; ALT_SEQ
R; S03604; S03604.
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CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: TYR-|-XAA.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY. BELONGS TO THE GLANDULAR KALLIKREIN SUBFAMILY.
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MIM; 176820; -...
PROSITE; PS00134; PROSITE; PS00135; PF00135; PF00089; LTY
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T -> I (IN REF. 5).
H -> T (IN REF. 9).
V -> M (IN REF. 8).
FLTP -> HLLYDOM (IN REF. 9).
D -> Q (IN REF. 9).
C -> Q (IN REF. 5).
C -> Q (IN REF. 5).
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seq_name: SwissProt_37:TRYB_RAT
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TRYB_RAT STAN
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01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
11-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TRYPSINOGEN V-B PRECURSOR (EC 3.4.21.4).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                EMBL: X59013; G57415; -.
PIR: JQ1472; JQ1472.
PROSITE: PS00135; TRYPSIN_SER;
PROSITE: PS00134; TRYPSIN_HIS;
PFAM; PF00088; trypsin; 1.
HSSP: P00763; 1DPO.
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL: D78203: G1805493: -.
EMBL: AF013988: G2318115: -
MIM: 602652: -.
                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                               "Zyme, a novel and potentially amyloidogenic enzyme cDNA isolated from Alzheiner's disease brain.";
J. BIOL. CHEM. 272:25135-25142(1997).
-!- SUBCELLULAR LOCATION: SECRETED.
-!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN BRAIN. ALSO FINE TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN BRAIN.
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LITTLE S.P., DIXON E.P., NORRIS F., BUCKLEY W., BECKER G.W.,
JOHNSON M., DOBBINS J.R., WYRICK T., MILLER J.R., MACKELLAR W.,
HEPBURN D., CORVALAN J., MCCLURE D., LIU X., STEPHENSON D.,
CLEMENS J., JOHNSTONE E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAMASHIRO K., TSURUOKA N., KODAMA S., TSUJIMOTO M., YAMAMURA TANAKA T., NAKAZATO H., YAMAGUCHI N.;
"Molecular cloning of a novel trypsin-like serine protease (n preferentially expressed in brain.";
preferentially expressed in brain.";
BIOCHIM. BIOPHYS. ACTA 1350:11-14(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PROTEASE M PRECURSOR (EC 3.4.21.-) (NEUROSIN)
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GluCysGluHisAlaTyrProGlyGlnIleThrGlnAsnMetLeuCysAl
                                  GTCTGCAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGC
                                                                       spPheProAspThrIleGlnCysAlaTyrIleHisLeuValSerArgGlu
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Search information block:
Query: US-09-030-606-173
Query length: 1265
Database: SPTREMBL_10:*
Database sequences: 201082
Database length: 61543640
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sp_mammal:Q29015
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-Q-/cgn2_1/USPT0_spool/US0903606/runat_24091999_171617_29869/app_query.fasta.1
-Q-/cgn2_1/USPT0_spool/US09036066/runat_24091999_171617_29869/app_query.fasta.1
-DB-SPTREMBL_10 -QFMT-fastan -SUOPCL-0.000
-GAPOEXT-4.000 -MINANTCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
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   O920ml mus musculus (mouse). en O75837 homo sapiens (human). se O63274 rattus norvegicus (rat). O63275 rattus norvegicus (rat). O63275 rattus norvegicus (rat). O63276 pleuronectes americanus. O929474 canis familiaris (dog). O93265 pleuronectes americanus. O92956 pleuronectes americanus. O92099 paranotothenia magellani. O42608 petromyzon marinus (sea. O42158 petromyzon marinus (sea. O42159 petromyzon marinus (deir). O42603 petromyzon marinus (sea. O42159 petromyzon marinus (deir). O42159 praomys natarensis (deir). O4683 ovis aries (sheep). mast (deir). O4683 ovis aries (deir). O
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    Quality:
    Ratio:
    Percent Similarity:
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sp_vertebrate:O13057 + 3
sp_invertebrate:O18599 +
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                                         GETCCTCTGCCCAGTCGCGGGGGGCTGACCCAGAGCTCTGCGTCCCAGGCA
                                                                                             yGlnLeuLysAsnGly..Lys.....
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seq_name: sp_rodent:Q920M1
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Q9Z0M1 PRELIMINARY;
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Q9ZOM1;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TrEMBLrel. 10, Last annotation update)
ENAMEL MATRIX SERINE PROTEINASE 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Enamel Matrix Serine Proteinase 1 (EMSP1).";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
EMBL; AF019979; AAC98894.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-SWISS-WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                     AGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATT
                                                                                                                                                                                           ACTGTTTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAG
                                                                                                                                                                                                                                                                                                           AGCCCGCACTCGCAGCCCTGGCAGGCGCACTGGTCATGGAAAACGAATT
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                                                                                 ysLeuAsnGluSerValIleGluSerAsnThrIleArgSerIleProVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 245
Gaps: 2
Percent Identity: 62.857
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513.27 4.1e-21
50 512.62 4.5e-21
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MATRIX SERINE PROTEINASE; 6E711616 CRC32;
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O13057 trimeresurus
i O18599 drosophila
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seq_documentation_block:
ID 075837
AC 075837
PRELIMINA
AC 075837
AC 07-8837
AC 01-NOV-1998 (TrEMBLre
DT 01-NAY-1999 (TrEMBLre
DE SERINE PROTEASE (TLSF
OS HOMO SAPIENS (Human).
OC EUKARYOTA; Metazoa; (
CC EUKARYOTA; Metazoa; (
CC EUKARYOTA; Metazoa; (
CC EUKARYOTA; PRIMATES; (
RN 520UENCE FROM N.A.
RX MEDLINE; 98438738.
RA YOSHIDA S., TANIGUCH;
RA YOSHIDA S., TANIGUCH;
RA YOSHIDA S., TANIGUCH;
RA 1-CDNA Cloning and exg.
RL Biochim. Biophys. Act
EMBL; AB01291; BAA3;
DR PFAM; PF00089; Tryps:
KW POTCHABE; Serine prot
CHAIN
SQ SEQUENCE 282 AA; :
                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                us-09-030-606-173 x 075837
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                                                                                                                                                                                    Align seg 1/1 to:
                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 075837;
01-NOV-1998 (TremBLrel. 08, C
01-NOV-1998 (TremBLrel. 08, I
01-MAY-1999 (TremBLrel. 10, I
SERINE PROTEASE (TLSP).
                                                                                                                                                                                                                                                                                                                                                                   YOSHIDA S., TANIGUCHI M., SUEMOTO T., OKA T., HE X.P., SHIOSAKA S.; "CDNA cloning and expression of a novel serine protease, TLSP."; Biochim. Biophys. Acta 1399:225-228(1998).
EMBL; AB012917; BAAA33404.1; PFAM; PF00089; trypsin; 1. Protease; Serine protease.
CHAIN 54 282 TLSP.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                              107 GTTTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCC 156
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                                                                                                                    CACTGAGTGGATAGAGAAAACCGTCCAGGCCAGT 737
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31059 MW;
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Percent Identity:
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seq_documentation_block:
ID_Q63274
AC Q63274;
AC Q63274;
AC Q63274;
AC Q63274;
DT 01-NOV-1996 (TrEMBLreDT 01-NOV-1996 (TrEMBLreDT 01-NOV-1998 (TrEMBLREDT 01-NOV-1998)
CRACTURERIN (FRAGMENT)
OS Rattus norvegicus (RacC Eukaryota; Metazoa; Cacce Eukaryota; Metazoa; Cacce Eukaryota; Modentia; SRN (1]
OC Eutheria; Rodentia; SRN (1]
RP SEQUENCE FROM N.A.
SCOURCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY
RA ZINTZ C.B., MA J.X.
RL Submitted (JAN-1995)
DR SEMBL; L33839; AAA5878
DR PFAM; PF00089; trypsi
SQ SEQUENCE 235 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                              seq_name: sp_rodent:Q63274
                                                          STRALM-SPRAGUE-DAWLEY: TISSUE-KIDNEY;
ZINTZ C.B., MA J.X., CHAO J., CHAO L.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ
EMBL; L33839; AAA58781.1;
                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                     01-NOV-1996 (TremBLrel.
01-NOV-1996 (TremBLrel.
01-NOV-1998 (TremBLrel.
KALLIKREIN (FRAGMENT).
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|sProGlyPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleM
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Last sequence update)
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alignment_scores:

Quality:

474.50

Length:

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alignment_block:
US-09-030-606-173 x Q63274
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnSerGlnProTrpGlnValAlaValIle.....AsnArgTyrLeuCy 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTG
                                                                                                                            pLysValThrAspLeuMetLeuCysAlaGlyLysLeuGluGlyGlyLysA
                                                                                                                                                                                                                                                                                                 GCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCCAAGACCAGAAGG 576
                                                                                                                                                                                                                                                                                                                                                               GTGAACGTGTCGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGACCC 526
                                                                                                                                                                                                                                                                                                                                                                                              CTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCTGCAGTGC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGG 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oAspTyrAsnProPheLeuMetArgAsnHisThrArgGlnThrGlyTyrA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...GluProPheAlaGlnTyrArgPheValSerGlnSerPheProHisPr 73
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                                                              oGlyIleTyrThrLysIleIleLysPheThrSerTrpIleLysGluValM
                                                                                                                                                                CAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCC 676
                                                                                                                                                                                                                                                                                                                                ValAsnIleAspLeuLeuSerAsnGluLysCysIleGluAlaTyrArgTr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....GCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAG 276
etLys 232
                               TCCAG 731
                                                                                              AGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCG 726
                                                                                                                                                                                                                               ACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTG 626
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64.822
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Percent Identity: 40.
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seq_name:

sp_rodent:Q63275

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alignment_block:
US-09-030-606-173 x Q63275
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Q63275 PRELIMI
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ZINTZ C.B., MA J.X., CHAO J., CHAO L.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L33840; AAA58782.1; -.
PFAM; PF00089; trypsin; 1.
NON_TER 1 1
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01-NOV-1996
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                136
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                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 CACTCGCAGCCCTGGCAGGCGCACTGGTCATGGAAAACGAATTGTTCTG
                                                                                                                                                                              GAACTCTTGCCTCGTTTCTGGCTGGGGGTCTGCTGGCGAACGGTGAGCTCA 376
                                                                                                                                                                                                                                                                                                                                                        oAspTyr...LysProPheLeuMetArgAsnH1sThrArgLysProLysA
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CGTGAACGTGTCGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGACC
                              ....SerThrAsnProSerGluTrpGluPheProAspAspLeuGlnCy
                                                              CTGACCCAGAGCTCTGCGTCCCAGGCAGAATG.CCTACCGTGCTGCAGTG
                                                                                                                               CGGGTGTGTGTCTGCCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGG
                                                                                                                                                            ySerThrCysLeuValSerGlyTrpGly......
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                                                                                             469.00
2.825
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Gaps: 6
Percent Identity: 39.286
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Last annotation update)
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US-09-030-606-173 x Q92046
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Ratio:
Percent Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Notothenioidei; Nototheniidae; Dissostichus.
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CHEN L., DEVRIES A.L.,
Submitted (MAY-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U58945; AAB57732.1; -. EMBL; U58835; AAB57728.1; -. FFAM; PF00089; trypsin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Hydrolase.
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                                                        SerProHisSerArgProTyrMetAlaSerLeuAsnTyrGlyTyrHis..
                                                                                                           AGCCCGCACTCGCAGCCCTGGCAGCCGCCACTGGTCATGGAAAACGAATT
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Percent Identity:
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EMBL/GenBank/DDBJ
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PROTRYPSIN.
55C59EB4 CRC32;
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seq_documentation_block:
ID Q29474
AC Q29474;
AC Q29474;
AC Q29476;
DT 01-NOV-1996 (TIEMBLIEL 01
DT 01-NOV-1996 (TIEMBLIEL 01
DT 01-NOV-1998 (TIEMBLIEL 01)
DT 01-NOV-1998 (TIEMBLIEL 02)
CALLIKREIN PRECURSOR (EC 2)
DE KALLIKREIN PRECURSOR (EO 2)
CE CALLINGEIN PRECURSOR (EX 2)
CE CALLICATION (KII
OS CANÍS familiaris (Dog).
CC EURALYOTA; METAZOA; Chorda'
CC EURALYOTA; Carnívora; Fissi;
RN [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MONGREL;
RR MEDLINE; 94250683.
RX MEDLINE; 94250683.
                                                                                                                                                                                                                                                                                                                                                                                   seq_name: sp_mammal:Q29474
                                                                                                                                                                   01-NOV-1996 (TIEMBLIFE! 01, Created)
01-NOV-1996 (TIEMBLIFE! 01, Last sequence update)
01-NOV-1998 (TIEMBLIFE! 08, Last annotation update)
KALLIKREIN PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN)
(GLANDULAR KALLIKREIN) (KININOGENIN).
                                                                                                          Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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pGlnGlnValCysGluAsnThrTyrProGlyLeuIleSerThrThrMetV
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Quality:
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Percent Similarity:
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LL Blochim. Blophys. Acta 1218:102-104(1994).
CC -I-CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF ARG-[-XAA BONDS IN SMALL MOLECULE SUBSTRATES.
CC HIGHLY SELECTIVE ACTION TO RELEASE KALLIDIN
CC (LYSYL-BRADYKININ) FROM KININOGEN INVOLVES HYDROLYSIS OF
CC MET-[-XAA OR LEU-[-XAA.
CC MET-[-XAA OR LEU-[-XAA.
CC THE RAT ENZYME IS UNUSUAL IN LIBERATING BRADYKININ DIRECTLY FROM AUTOLOGOUS KININOGENS BY CLEAVAGE AT TWO ARG-[-XAA BONDS.
CC AUTOLOGOUS KININOGENS BY CLEAVAGE AT TWO ARG-[-XAA BONDS.
CREMBL; X75479; CAA53210.1;
CREMBL; X75479;
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spTyrSerHisAspIleMetLeuLeuArgLeuAlaGluProAlaGlnIle 132
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                                                                     ValAspLeuGluLeuLeuSerAsnAspIleCysAlaAsnAlaHisSerGl 190
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GCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGG
                                                                                                                                                                                                                                                                                      CTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCTGCAGTGC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oGluPheAsnLeuSerLeuLeuLysAsnHisThrArgLeuProGluGluA 116
                                                                                                                                       GTGAACGTGTCGGTGTCTCAGGAGGTCTGCAGTAAGCTCTATGACCC
                                                                                                                                                                                                         .....ProAspLysPheIle......TyrProAspAspLeuGlnCys 173
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261 AA;
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                  DOUGLAS S.E., GALLANT J.W.;
"Isolation of CDNAs for Trypsinogen
Pleuronectes americanus."
J. Mar. Biotechnol. 0:0-0(1998).
EMBL; AF012462; AAC32751.1;
PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pleuronectes.
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                       154 GCCGACCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACG
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                                                  rpTyrAsnProTyrAlaMetGlnValMetLeuGlyGluHisAsnLeuArg
                                                                                                      CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT
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Val...PheGluGlyThrGluGlnLeuMetLysThrAspThrIleIleTr
                                                                             TCCAGAACTCCTACACC....ATCGGGCTGGGCCTGCACAGTCTTGAG
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Last annotation update)
3.4.21.4).
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TRYPSINOGEN 1.
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Seq_documentation_block:
ID 088309
AC 088309
DT 01-NOV-1998 (TrEMBLrel 08
DT 01-NOV-1998 (TrEMBLrel 08
DT 01-NAY-1999 (TrEMBLrel 08
DT 01-MAY-1999 (TREMBLR)
OE PRORENIN-CONVERTING ENZYME
GN MKIK-13B.
OC Eukaryota; Metazoa; Chorda
OC Eutheria; Rodentia; Sciuro
RN (1)
RE SEQUENCE FROM N.A.
RX MEDLINE; 98351995.
RA HOSOI K., TADA J., TSUMURA
RT "Expression of an allozyme
RT submandibular gland of DBA
RL J. Blochem. 124:368-376(19
DR EMBL; AB016032; BAA31686.1
DR PFAM; PF00089; trypsin; 1.
KW Signal.
SEQUENCE 261 AA; 28692
                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_rodent:088309
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TREMBLECI. 10, Last annotation update)
prorenin-Converting Enzyme (MK13B) PRECURSOR (MK13B).
                                                          MEDLINE; 98351995.

HOSOI K., TADA J., TSUMURA K., KANAMORI N., YAMANAKA N.;
"Expression of an allozyme of prorenin-converting enzyme
submandibular gland of DBA/2N mice.";
J. Blochem. 124:368-376(1998).
EMBL; AB016032; BAA31686.1; -.
PFAM; PF00089; trypsin; 1.
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                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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alignment_scores:

Quality:

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Length:

252

seq_name:

sp_rodent:Q61855

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alignment_block:
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Percent Similarity:
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50 sGlyGlyValLeuLeuAspArgAsnTrpValLeuThrAlaAlaHisCysT
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                                                           oAlaIleTyrThrAsnLeuIleLysPheAsnSerTrpIleLysAspThrM
                                                                                       AGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCG
                                                                                                                                                                               ACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGATCTGCAACGGGTACTTG
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Percent Identity:
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seq_documentation_block:
ID Q61855
AC Q61855
DT Q1.NOV-1996 (TrEMBLTel. 0)
DT Q1.NOV-1996 (TREMBLTel. 0)
DT Q1.ANN-1999 (TREMBLTel. 0)
DT Q1.ANN-1999 (TREMBLTel. 0)
DE TISSUE KALLIKREIN.
GN MGK-6.
OS MUS MUSCULUS (MOUSE).
QC EUKARTYOTA; Metazoa; Chorda
QC EUKARTYOTA; TAKAH; RT TADA M., PETERS J., TAKAH;
RT TADA M., PETERS J., TAKAH;
RT TADA M., PETERS J., TAKAH;
RT TADA M., PETERS J., TAKAH;
RT TADA M., PETERS J., TAKAH;
RT TOOLSE neuroendocrine cell
RL Submitted (JUN-1991) to tl
DR EMBL; D10464; BAA01257.1;
DR PFAM; PETO0089; trypsin; 1
DR PFAM; PETO0089; trypsin; 1
DR PFAM; PETO0089; trypsin; 1
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US-09-030-606-173 x Q61855
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"Identification of a tissue kallikrein gene, mGK-6, expumouse neuroendocrine cell line.";
Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases EMBL; D10464; BAA01257.1; -.
PFAM: PF00089; trypsin; 1.
SEQUENCE 261 AA; 28775 MW; 509D1D00 CRC32;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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seq_documentation_block:
ID 093266
AC 093266;
DT 01-NOV-1998 (TrEMBLrel 08
DT 01-NOV-1998 (TrEMBLrel 108
DT 01-NAY-1999 (TrEMBLrel 108
DT 01-MAY-1999 (TrEMBLrel 108
DT 01-MAY-1999 (TREMBLREL 100
DE TRYPSINOGEN 2 PRECURSOR (E
GN TRP2.
CC Eukaryota; Metazoa; Chorda
CC Eukaryota; Metazoa; Chorda
CC Pleuronecttiformes; Pleuron
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=INTESTINE, PYLORIC
RA DOUGLAS S.E., GALLANT J.W.
RT TISSUE=INTESTINE, OF COMAS for TR
RT TISSUE=INTESTINE, OF COMAS FOR TR
RT TISSUE=INTESTINE, PYLORIC
RA DOUGLAS S.E., GALLANT J.W.
RT TISSUE=INTESTINE, PYLORIC
RA DOUGLAS S.E., GALLANT J.W.
RT TISSUE=INTESTINE, PYLORIC
RA DOUGLAS S.E., GALLANT J.W.
RT TISSUE-INTESTINE, PYLORIC
RA DOUGLAS S.E., GALLANT J.W.
RT TISSUE-INTERSTINE, PYL
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Quality:
Ratio:
Percent Similarity:
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EMBL; AF012463; AAC32752.1; -.
PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOUGLAS S.E., GALLANT J.W.;
"Isolation of cDNAs for Trypsinogen
Pleuronectes americanus.";
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                          104 ACTGTTTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAG
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                                                                                         43 sPheCysGlyGlySerLeuValAsnGluAsnTrpValValSerAlaAlaH
                                                                                                                          54 GTTCTGCTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCAC
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seq_name: sp_vertebrate:Q92099
GENICOT S., RENTIER-DELRUE F., EDWARDS D., VAN BEEUMEN J., GERDAY C.; "Trypsin and trypsinogen from an Antarctic fish: molecular basis of cold adaptation."; Blochim. Brophys. Acta 1298:45-57(1996).

EMBL; X82223; CAA57701.1; -.
                                                                                                                                                                                               Paranotothenia magellanica.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Acanthopterygil; Percomorpha;
Perciformes; Notothenioidei; Nototheniidae; Paranotothenia.
                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 00, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
TRYPSIN PRECURSOR (EC 3.4.21.4) (ALPHA- AND BETA-TRYPSIN).
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......AspLeuLeuGlnCysLeuAspIleProIleLeuSerPheSer 165
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US-09-030-606-173 x Q92099
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SIGNAL 1
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                                        ...CysAlaGluArgAspHisProGlyValTyrAlaLysValCysLeuPh
                                                                             CCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATT
                                                                                                                    roValValCysAsnGlyGluLeuGlnGlyValValSerTrpGlyTyrGly
                                                                                                                                                        CCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCC
                                                                                                                                                                                             aGlyTyrLeuGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyP
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26201 MW;
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Percent Identity: 38.430
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US-09-030-606-173 x 054854
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SCARISBRICK I.A., TOWNER M.D., ISACKSON P.J.;

"Nervous system-specific expression of a novel serine protease: regulation in the adult rat spinal cord by excitotoxic injury.";

J. Neurosci. 17:8156-8168(1997).

EMBL; AF016269; AAC02300 1; -.
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01-JUN-1998 (TERMBLTEL. 06, Last sequence update)
01-MAY-1999 (TERMBLTEL. 10, Last annotation updat
MYELENCEPHALON SPECIFIC PROTEASE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammali
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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CCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGCTGACCCAGAGCTCT
                                                                                                                                                                                                                                                                                       AGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCCTCGT 341
                                                                                                                                                                                                                                                                                                                                                                                                    TCATGCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCCATCCGG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pArgThrIleValHisProArgTyrAsnProGlnThrHisAspAsnAspI 114
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eAsnAspTrpLeuGluThrSerMet
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                                                                                                                                       ProLeuProLeuLysLysAspCysSerGluLysAsnProAspCysGlnIl 147
                                                                                                                                                                                                                                                                                                                                                       leMetMetValH1sLeuLysArgProvalLysPheSerGlnArgIleGln 130
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Seq_documentation_block:
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DT 01-JAN-1998 (TrEMBLEE
DT 01-JAN-1998 (TrEMBLEE
DT 01-OV-1998 (TrEMBLEE
DT 01-OV-1998 (TREMBLEE
DE TRYPSINOGEN A3 PRECUM
GN TRYPA3.
OS Petromyzon marinus (S
OC Eukaryota; Metazoa; C
OC Petromyzontiformes; F
RN [1]
RP SEQUENCE FROM N.A.
RA ROACH J.C.;
RL Submitted (SEP-1997)
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ANTERIOR INTES
RA ROACH J.C.;
RA ROACH J.C.;
RA ROACH J.C.;
RA SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
GEQUENCE FROM N.A.
GEQUENCE FROM N.A.
SIGNAL J.C.;
SUBMITTED (AUG-1997)
DR EMBL; AFO11899; AAB659
DR EMBL; AFO11892; AAB659
DR EMBL; AFO11892; AAB65
DR PFAM; PFO0089; TrYPS1
KW Signal 1
FT CHAIN
SQ SEQUENCE 247 AA; 24
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US-09-030-606-173 x 042608
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                                                                                                                  Align seg 1/1 to: 042608
                                                                                                                                                                                                                  Percent Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Cephala:
Petromyzontiformes; Petromyzontidae; Petromyzon
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01-JAN-1998 (TrEMBLrel. 05, Last seg
01-NOV-1998 (TrEMBLrel. 08, Last ann
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TISSUE-ANTERIOR INTESTINE;
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                                     \omega
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                                                        CACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTG
CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT
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                                   HisSerGlnProTrpGlnValSerLeuAsnIleGlyTyrHis...PheCy
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247
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Gaps: 6
Percent Identity: 36.327
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seq_documentation_block:
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AC 042158;
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DT 01-7AN-1998 (TREMBLrel. 05, Last sequen
DT 01-NOV-1998 (TREMBLrel. 08, Last annota
DE TRYPSINOGEN A2 PRECURSOR.
GN TRYPA2.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata;
OC Petromyzontiformes; Petromyzontidae; Pe
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RA ROACH J.C.;
RL SUBMITTED (JUL-1997) to the EMBL/GenBan
DR EMBL; AF011898; AAB69654.1; -.
DR PFAM; PF00089; trypsin; 1.
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                                                                                                                 Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Cephalaspidomorphi;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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                                          EMBL/GenBank/DDBJ databases
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US-09-030-606-173 x 042158
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Ratio:
Percent Similarity:
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Signal
CHAIN
SEQUENCE
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nHisProGinTyrAsnSerTrpThrIleAspAsnAspIleMetLeuIleL
CACTGAGTGGATAGAGAAAACCGTCCAGGCCAGT
                                                     CCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATT
                                                                                  roValValCysAsnGlyGluLeuGlnGlyIleValSerTrpGlyArgGly
                                                                                                              CCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCC
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Pred. No.

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                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F.
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequenci Clone distribution: NCI-CGAP clone distribution informat found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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nj43ell.sl NCI_CGAP_Pr9
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Unpublished (1997)
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1 (bases 1 to 435)
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National Cancer Institute, Cancer Genome Anatomy
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agarose gel,
D. Krizman, N
                                                  /note="Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                        /organiam="Homo sapiens"
/db_xref="taxon:9606"
/map="902809; 2; 2p11.2-2p13.1"
/clone="IMAGE:995276"
                                                                                                                                     /tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
                                                                                                                                                                  /clone_lib="NCI_CGAP_Pr9"
/sex="male"
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        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1393204"
/clone_lib="Soares_testis_NHT"
/sex-"male"
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Query Match

Score 363.4;

DВ 38 ;

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2 CTCTTTCTCTCCCCTCTGTAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACAC
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro Tumor Gene Index
Unpublished (1997)
On Apr 18, 1995 this sequence version replaced gi:77
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aj44g03.sl Soares_testis_NHT
                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
               Insert Length: 982 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 503.
                                                                                                        ₩ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                        DNA Sequencing by: Washington University Genome Sequencing Cente Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                            cDNA Library Arrayed by: Greg Lennon,
Location/Qualifiers
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                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washd-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                          AA437224 490 bp mRNA EST 30-MAY-1997 zv54b10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757 3' similar to contains Alu repetitive element;, mRNA sequence. AA437224
Contact: Wi
Washington
                                                 Unpublished (1997)
On Sep 12, 1996 th
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AA437224.1 GI:2142138
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                Wilson RK
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech was prepared from mRNA obtained with a Not I - oligo(dT)
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99.78;
                                                   this sequence
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Pred. No. 2.6e-71;
0; Mismatches 0;
 School of
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GTTCTCAGAACCATTTCACCCAGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGG 298
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mRNA sequence.
AI685682
g4896976
                                              AI685682 423 bp n
tt89h03.x1 NCI_CGAP_Pr28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Seq primer: -41nl3 fwd. ET from Amersham High quality sequence stop: 363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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/db_xref="GDB.5978049"
/db_xref="taxon:9606"
/map="6 p23-p22; 949D05; 2
/clone="IMAGE:757435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_testis_NHT"
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99.2%;
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Homo sapiens cDNA
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7.7e-71;
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                                                   clone IMAGE:2248757
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183
                               265 GCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCCTG
                                                                                                                                           243 CTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATTTCACCCAGACA 184
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   GCCTGTTTCTATCCTGTTTAATAAATTAGTTTTGGGTTCTCTACATGCATAACAAACCCTG
                                                                                                                                                                                          CTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATTTCACCCAGACA 264
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Location/Qualifiers
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1 (bases 1 to 423)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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//lab_host="DHIOB"
//lab_host="DH
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/map="19p12-p13.1"
/clone="IMAGE:2248757"
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/sex="male"
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Query Match
Best Local S
Matches 325
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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g1851569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 856 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 368.
Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Sep 12, 1996 this sequence version replaced gi:1394602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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                       Similarity
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                                                                                                                                                  141
  Conservative
                                                                                                                                        /note="vector: pampl0; Site_1: Not1; Site_2: EcoRI; 1st /note="vector: pampl0; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pampl0 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                  D
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1010092"
/clone_11b="NCI_CGAP_Pr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                    85.5%;
99.4%;
0
                    Score 313; DB 30;
Pred. No. 5.6e-62;
Mismatches
0;
                                           Length 419;
Indels
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Gaps
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Length 411;

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288 184 228 124

244

is 600 bp. NOTE: was constructed 1

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JOURNAL COMMENT
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Unpublished (1997)
On Dec 30, 1996 th
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nr28d08.rl NCI_CGAP_Pr3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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1 (bases 1 to 411)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                    primer: -28m13 rev1 ET from Amersham
h quality sequence stop: 387.
    Location/Qualifiers
/dev.stage="45 years old"
//lab_host="DH10B"
//lab_host="DH10B"
//lab_host="Net10: Site_1: Not1; Site_2: EcoRI; Ist
//note="Vector: pAMP10; Site_1: Not1; Of ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected cells
histologically-determined to be fully malignant prostate
cancer cells. Double-stranded cDNA was ligated to EcoRI
adaptors, 5 cycles of PCR applied to the cDNA with an
adaptor-specific primer, and the resulting PCR product
subcloned into pAMP10 by the UDG-cloning method (Life
                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Pr3"
/sex="Male"
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1169295"
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                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94852484
AI672753.1
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Unpublished (1997)
On May 18, 1998 th
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 383)
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                                                                                                                                                                                     IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                     High quality sequence stop: 362
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nilarity 99.4%;
Conservative
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directionally c
David Krizman.
a 80 c 6
                                        /map="952F05; 14; 14q23.1-14q24.1;
MMU16C3-C4 region"
/clone="IMAGE:2345299"
   /clone_lib="Soares_thymus_NHFTh"
/dev_stage="fetal"
                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                  1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:4852484
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18-MAY-1999

element;, mRNA

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AA533772/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTAGTC 366
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                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                     On May 8, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.

1 (bases 1 to 445)
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AA533772
Insert Length: 613
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National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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Pred. No. 8.5e-59;
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IMAGE:1000040,
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                                                                                                                                                                                                                                                                             sequence.
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Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Li
                                                                        Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version
                                                                                                                      1 (bases 1 to 423)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AA531606.1
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nj65e04.sl NCI_CGAP_Pr10
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quality sequence stop: 317.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1000040"
/clone_lib="NCI_CGAP_Prll"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="normal prostatic epithelial cells"
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98.5%;
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W. Marston Linehan, M.D.,

Rodrigo F. Chuaqui,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                              AA493522 403 bp
ng75f05.sl NCI_CGAP_Pr6
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quality sequence stop: 319.
   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: prostate; Vector: pAMP10; mRNA made from invasive prostate tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Pr10"
/sex="male"
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/db_xref="taxon:9606"
/clone="IMAGE:997374"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="invasive prostate tumor"
/lab_host="DH10B"
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97.8%;
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Matches 300; Conserv
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                                                                                                                                        TT 301
AA650104 339 bp mRNA EST 13-NOV-1997 ns92f11.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1191117, sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: David G. Bostwick, M.D., Rodr M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Clone distribution: NGL-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Jun 18, 1996 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 651
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                                                                                                             403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pAMP10; mRNA made from prostatic intraepithelial neoplasia (low-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:940641"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="prostate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Pr6"
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99.38;
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Best Local Similarity
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                                                                    122 TGGTTTGTGAATCCATCTTGCTTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAA 181
    182 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTT
                                                                                                                                      62 ATTTCACTGTGATGTATATTGTGTTGCAAAAAAAAAAAGTGTCTTTGTTTAAAATTACT 121
                                                 TGGTTTGTGAATCCATCTTGCTTTTTCCCCCATTGGAACTAGTCATTAACCCATCTCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA650104
g2577432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Sep 1, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index 
Unpublished (199)
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1 (bases 1 to 339)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert Length: 1362
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National Cancer Institute, Cancer Genome Anatomy
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quality sequence stop: 291.
   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was lighted to EORI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              David Krizman.
72 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/map-"17921; between D17S1321 and D17S1325"
/clone-"IMAGE:1191117"
/clone_1ib-"NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="45 years old"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                           77.78;
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                                                                                                                                                                                                                                                                                                                                           Score 284.2; DB 36; Length Pred. No. 2e-55;
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  75 GTATATTGTGTTGC-AAAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAAT 133
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
Chun Tiber: Proceedings of the Ph.D.
Chun Tiber: Proceedings of the Ph.D.
Chun Tiber: Proceedings of the Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Gibco.
Location/Qualifiers
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On Dec 20, 1995 this sequence version replaced gi:1130922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 377)
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AI669511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                Conservative
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                                                                                                                                                                         /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was perpared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.

a 61 c 74 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2312773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib-"NCI_CGAP_Pr28"
                                                                   76.8%; Score 281; DB 50; Length 377; 99.7%; Pred. No. 1e-54;
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                                                0;
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W47380.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 374)

1 (lbases 1 to 374)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rohlfing,T., Soares,M., Tan,F., Rohlfing,T., R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq_primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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   /Clone_"IMAGE:324741"
/Clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:1256253"
/db_xref="taxon:9606"
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Query Match

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DB 26;

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TATATTGTGTTGC-AAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGTAAATC 134
                                                                                  CACCCAGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATA 314
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                                                                                                                                                                                                                                                                                      Conservative
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Search completed: September 25, 1999, 12:05:07 Job time: 8111 sec

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A_Geneseq_36: W91871
A_Geneseq_36: W91873
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A_Geneseq_36: W95388
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A_Geneseq_36: W136086
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-MODEL-frame+_n2p.model -DEV=xlp
-O-/Ggn2_1/USPT0_spool/US09030606/runat_24091999_171616_29804/app_query.fasta.1
-OB-A_Geneseq_36 -OFMT-fastan -SUFFIX=rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH-0.100 -LOOPEXT=0.000 -LOOPEXT=0.000
-OGAPOP-4.500 -OGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -START=1 -MATRIX-blosum62
-TRANS-humman40.0d1 -LIST=45 -DOCALIGN=200 -THR_SCORE-escore
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM-stat -USER-US09030606
-NCPU-6 -ICPU-3 -WAIT -THREADS=1
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Query length: 1265
Database: A_Geneseq_36:*
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Database length: 23686106
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A_Geneseq_36:W69388
A_Geneseq_36:W71872
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                                                                          Human stratum corneum chymotrop Human amyloid precursor protein Human amyloid precursor protein Human mecombinant neuropsin, waclei Human recombinant neuropsin, waclei A human serine protease designa Mature prostate-specific glandular kal prostate-specific antigen protease-specific antigen protease pro-hk2 kallikrein. New isolate prepro-hk2 kallikrein. New isolate prepro-hk2 kallikrein specific antige protease My a novel serine protease. Amy Human prostatic specific antige tyme App-cleaving protease. Amy Human serine protease 59 (Sp59) protease My a novel serine protease Mutant human kallikrein 2 (hk2) hk2 variant A217v. Detection of
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                      hK2 variant A217V. Detection of Variant human Kallikrein 2 (hK Kallikrein prepro-hK2v217 vari
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A_Geneseq_36:R77098
A_Geneseq_36:W03130
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US-09-030-606-173
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                            CTTGAGGCCGACCAAGAGCCAGGGGAGCCAGATGGTGGAGGCCAGCCTCTC
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Quality:
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seq_documentation_block:
ID W59129;
AC W59129;
PT 11-SEP-1998 (first entry)
DE Homo sapiens Tub Interactor
KW serine protease; tub interactor
KW parkinson's disease; Hunting
KW parkinson's disease; PS (laim 28; Fig 1; 120p; Engl
CC pin biochemical pathways invo
CC pin biochemical pathways invo
CC weight disorders, e.g. obesi
CC or a related disorder such a
also be used to modulate cel
CC They can be used for treatin
CC weight disorders, e.g. obesi
CC or a related disorder such a
also be used for treatin
CC weight disorders, e.g. obesi
CC or a related disorder such a
also be used for treatin
CC winch are characterised by a
CC disease, parkinson's disease
CC lateral sclerosis or spinoce
CC products can also be used fo
CC drug screening.
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                                                                                                                                                                                                                       diabetes
Claim 28; Fig 1; 120pp; English.
Chaim 29; Fig 1; 120pp; English.
Chaim 29; Fig 1; 120pp; English.
Chaim 29; Fig 1; 120pp; English.
Chaim 20; Fig 1; 120pp; 
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17-SEP-1996; US-715032.
(MILL-) MILLENNIUM PHARM INC.
ETTAGA PR. Gimeno CJ;
WPI: 98-217246/19.
N-PSDB; V11855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tub interactor genes - used to develop products for the treatment of obesity, cachexia, anorexia nervosa or related disorders e.g.
: 1109.50
: 4.975
: 87.451
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Length: 255
Gaps: 3
Percent Identity: 86.667
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Prostate-specific antigen.
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seq_documentation_block:
ID W60592 standard; Prot
AC W60592
DT 07-SEP-1998 (first e
DE Human prostate-specific kal
KW Prostate-specific kal
KW benign prostate hyper
OS Homo sapiens. Locat
FH Key Locat
FT Misc_difference 113
FT Misc_difference 128
FT Misc_difference 130
FT Mi
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                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate-specific kallikrein (HPSK) protein.
Prostate-specific kallikrein; HPSK; prostate carcinoma;
benign prostate hyperplasia; diagnosis; drug screening;
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                                                                                                                     /label=
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                                                                                                                                                                                                                                                                                                   ′label= unknown
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alignment_scores:
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Percent Similarity:
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(INCY:) INCYTE PHARM INC.
Bandman O, GO11 SK;
WPI; 98-286933/25.
N-PSDB; V37495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperplasia
Claim 1; Fig 1A-C; 68pp; English.

This represents a human prostate-specific kallikrein (HPSK). A host cell rontaining an expression vector comprising the HPSK nucleic acid sequence can be used to produce the protein recombinantly. The HPSK products can be used for the diagnosis of conditions or diseases associated with expression of HPSK such as prostate carcinoma and benign prostate expression of HPSK such as prostate carcinoma and benign prostate hyperplasia. Agonists and antagonists which specifically bind to HPSK and modulate its activity can be used for the preparation of treatment of such conditions or diseases. The products can also be used for detection and drug screening, especially for the detection of prostate-specific kallikrein (PSK).
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                            ACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTTCG
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AGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGG
                                                                                                                             CTGCCCAGTCGCGGGGGCTGACCCAGAGCTCTGCGTCCCAGGCAGAATGC
                                                                                                                                                       u..........
                                                                                                                                                                                            GGCGAACGGTGAGCTCACGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCT
                                                                                                                                                                                                                                                                                      spGluSerValSerGluSerAspAsnIleArg***IleSerIle***Ser
                                                                                                                                                                                                                                                                                                                                                      oGluTyrAsnArgProLeuLeuAlaAsnAspLeuMet***IleLysLeuA
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Ratio: 5.077
milarity: 87.654
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248 AA;
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alignment_block:
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Quality:
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Percent Similarity:
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27-AUG-1998.
25-FEB-1998; U03690.
09-FEB-1998; US-904809.
25-FEB-1997; US-806596.
01-AUG-1997; US-806596.
01-AUG-1997; US-806899.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _documentation_block:
                                                                                                                                                                                                                       Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers

Example 1; Page 115-116; 141pp; English.

This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     710
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N-PSDB; V58647.
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5.032
87.124
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seq_documentation_block:
ID W71872
AC W71872
DT O6-JAN-1999 (first e
DE Protein encoded by pir
KW Prostate; cancer; tum
OS Homo sapiens. Locat
FT Misc_difference 127
FT Misc_difference 204
FT W9837093-A2.
PD 27-AUG-1998. U03492.
PR 09-FEB-1998; U03492.
PR 09-FEB-1998; US-02095
PR 01-AUG-1997; US-90480
PA (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                     seq_name: A_Geneseq_36:W71872
27-AUG-1998.
27-AUG-1998.
25-FEB-1998; US-020956.
09-FEB-1998; US-020956.
25-FEB-1997; US-806099.
01-AUG-1997; US-904804.
(CORI-) CORIXA CORP.
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                                                                                                                                                                              06-JAN-1999 (first entry)
                                                                                                                                                                                                      W71872 standard; Protein; 205
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                                                                                                                     Location/Qualifiers
                                                                                                                                                                  by prostate tumour
                                                                                   /note-
                                                                                                        note-
                                                                                                         "undefined residue"
                                                                                                                                                       vaccine;
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                                                                                                                                                                   clone P703
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alignment_scores:
Quality: 1021.50
Ratio: 5.032
~'~'arity: 87.124
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WPI; 98-609886/51.
Polypeptides comprising immunogenic portions of prostate proteins -
used in a vaccine for the treatment of prostate cancer
Example 3; Page 107-108; 130pp; English.
The present sequence is an immunogenic portion of a prostate tumour
protein. The immunogen, or the DNA encoding it, can be used as a
vaccine for the treatment of prostate cancer. The immunogen was
isolated from a prostate tumour cDNA library obtained by subtracting
a prostate tumour cDNA expression library with a normal tissue cDNA
library.
The immunogen was serviced from the prostate cancer of the prostate tumour cDNA library with a normal tissue cDNA
library.
The immunogen immunogen was serviced from the prostate tumour cDNA library with a normal tissue cDNA
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                    ValSerGlyTrpGlyLeuLeu.....
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CTTTCGGAAAAGCCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACC
                                                                                                                                                                                                                        GCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGGCTGACCCAGAGCT 439
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Gaps:
Percent Identity:
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seq_documentation_block:
ID W69387;
AC W69387;
DT O8-DEC-1998 (first e DE Prostate tumour speci KW Prostate PN Misc_difference 103
FT Misc_difference 105
FT Misc_difference 105
FT Misc_difference 105
FT Misc_difference 105
FT Misc_difference 103690.
PR 09-FEB-1998; U3-90480
PR 09-FEB-1998; U3-90480
PR 01-AUG-1998; U3-90480
PR 01-AUG-1997; U3-90480
PR 01-AUG-1997; U3-90480
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PR 01-AUG-1997; U3-90480
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25-FEB-1998; U3690.
09-FEB-1998; US-904809.
25-FEB-1997; US-806596.
01-AUG-1997; US-904809.
(CORI-) CORIA CORP.
Dillon DC, Xu J;
WFI; 98-480805/41.
N-PSDB; V58644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers
Example 1; Page 112-113; 141pp; English.

This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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Prostate tumour specific gene; human; prostate cancer; detection;
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                                                                                                                                                                                                                                                                                              GCTCGCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAGT
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                                                                                                                            erAspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGly
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US-09-030-606-173 x W71871

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alignment_scores:
Quality:
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   Percent Similarity:
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25-FEB-1998; UG-020956.
09-FEB-1997; UG-806099.
01-AUG-1997; UG-904804.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9837093-A2.
                                                                                                                                                                     Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer Example 3; Page 105; 130pp; English.

The present sequence is an immunogenic portion of a prostate tumour protein. The immunogen, or the DNA encoding it, can be used as a vaccine for the treatment of prostate cancer. The immunogen was isolated from a prostate tumour cDNA library obtained by subtracting
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                                                                                                               a prostate tumour cDNA expression library.
Sequence 159 AA;
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Dillon DC, Xu J;
WPI; 98-609886/51.
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6 ||GlnAlaSer 159
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                   WO9837418-A2.
27-AUG-1998: U03690.
25-FEB-1998: US-904809.
09-FEB-1998: US-904809.
25-FEB-1997: US-806596.
01-AUG-1997: US-904809.
(CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 164 AA
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seq_documentation_block:
ID W71873 standard; Pro
AC W71873;
DT " 06'-JAN-1999 (first
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                                                                                     seq_name: A_Geneseq_36:W71873
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                  W71873 standard; Protein; 164 W71873;
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Example 1: Page 117-118; 141pp; English.

This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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N-PSDB; V58648.
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                                                                                                                             SerCysCysIleLeuThrGlyCysSerLeuLeuLeuThrAlaSer
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                                                                                                                                                                 CCGTGCTGCAGTGCGTGAACGTGTCGGTGTCTGAGGAGGTCT
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Ratio:
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alignment_block:
US-09-030-606-173
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Percent Similarity:
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25-FEB-1997; US-806099.
01-AUG-1997; US-904804.
(CORI-) CORIXA CORP.
D111on DC, Xu J;
WPI; 98-609886/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer Example 3; Page 109; 130pp; English.

The present sequence is an immunogenic portion of a prostate tumour protein. The immunogen, or the DNA encoding it, can be used as a vaccine for the treatment of prostate cancer. The immunogen was isolated from a prostate tumour cDNA library obtained by subtracting a prostate tumour cDNA library with a normal tissue cDNA library.
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                                                                                                                                                                            TGCACAGTCTTGAGGCCGACCAAGAGCCAGGGGAGCCAGATGGTGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGTCAGCCGCACACTGTTTCCAGAACTCCTACACCATCGGGCTGGGCC
lnProTrpGlnGlyCysThrIleSerAlaThrSerSerAlaArg..
                            CCCAGTCGCGGGGGCTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTA
                                                          r***ThrValGlyGlyTrpGluCys......
                                                                                                                     ValSerGlyTrpGlyLeuLeuAlaAsnAspAlaValIleAlaIleGlnSe 117
                                                                                                                                                GTTTCTGGCTGGGGTCTGCTGGCGAACGGTGAGCTCACGGGTGTG....
                                                                                                                                                                                                                                                                                                   AGCCTCTCCGTACGGCACCCAGAGTACAACAGACCCTTGCTCGCTAACGA
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Gaps: 3
Percent Identity: 73.333
                                                                                       TGTCTGCCCTCTTCAAGGAGGTCCTCTG
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463

CCGTGCTGCAGTGCGTGAACGTGTCGGTGTGTCTGAGGAGGTCT

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seq_documentation_block:
ID W94493
AC W94493
DT 23-APR-1999 (first e
DE Human kallikrein.
KW Human; kallikrein; ke
psoriasis; scleroderm
OS Homo sapiens
PN W09842849-Al.
O1-OCT-1998.
PF 25-MAR-1999; U05939.
PF 26-MAR-1997; U5-82487
PA (INCY-) INCYTE PHARM
PI Hillman JL, Lal P;
DR WPI; 99-070073/06.
DR N-PSDB; X16295.
PT disorders e.g. ezzeme
PT disorders e.g. ezzeme
PT disorders schin disorde
PS Claim 1; Page 41-42;
CC The present sequence
CC HKALL (or fragments)
CC e.g. ezzema, psoriasis
CC e.g. ezzema, psoriasis
CC structures necessary
CC of skin are eliminate
CC structures necessary
CC of skin are eliminate
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US-09-030-606-173 x
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CHKALL antagonists can be used to suppress excessive proteolysis and subsequent skin cell scaling, so may be administered to treat skin clisorders. They may also be used to suppress excessive cell disorders. They may also be used to suppress excessive cell proliferation, so can be administered to treat/prevent cancer, e.g. adenocarcinoma, leukaemia and melanoma. Antibodies specific for HKALL may be used directly as antagonists, or indirectly as a targeting or delivery mechanism for bringing pharmaceutical agents to HKALL-expressing cells. They are also useful to diagnose conditions/diseases characterised by HKALL expression and to monitor therapeutic interventions. The polynucleotide encoding HKALL, or complementary sequences, can be used to produce hybridisation probes, useful to detect polynucleotides encoding (e.g. cancers of the bladder, prostate) or monitor HKALL regulation during therapeutic intervention. Polynucleotides encoding HKALL are useful to produce antisense sequences for therapeutic administration to modulate/prevent HKALL expression e.g. to treat/prevent skin disorders or cancer as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders e.g. eczema, psoriasis and screen for antagonists useful to treat skin disorders and cancers Claim 1; Page 41-42; 6lpp; English.
The present seminance recognitions and seminance recognitions.
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Hillman JL, Lal P;
WPI; 99-070073/06.
N-PSDB; X16295.
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psoriasis; scleroderma; adenocarcinoma; leukaemia; melanoma.
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26-MAR-1997; US-824874.
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                72
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                                                                            72 GGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTTTCCAGAACTCCT
                                                                                                                                                                                                     CAGGCGGCACTGGTCATGGAA...AACGAATTGTTCTGCTCGGGCGTCCT
GlnAlaAlaLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLe
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3.277
70.293
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Percent Identity:
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seq_name: A_Geneseq_36:R67888
                                            (SYMB-) SYMBICOM AB.
Egelrud T, Hansson I
WPI; 95-052088/07.
N-PSDB; Q81203.
                                                                                                                                                                                                                                                                                                                                                       documentation_block:
                                                                                                                                                                                                                          Human stratum corneum chymotrophic recombinant enzyme (SCCE). Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides,
                                                                                                                                                                                      Homo sapiens.
W09500651-A.
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                                                                                                                          20-JUN-1994; IB0166.
18-JUN-1993; DK-000725.
                                                                                                                                                                     05-JAN-1995.
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                                                                                                                                                                                                                                                                                                                             R67888 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                     262 uThrIleGlnAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           722 AACCGTCCAGGCCAGT 737
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rr gooddoo

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alignment_block:
US-09-030-606-173 x R67888
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.

Disclosure; Page 97; 137pp; English.

The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507.

Sequence 253 AA;
  204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 GlyAlaProCysAlaArgGlySerHisProTrpGlnValAlaLeuLeuSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    euMetLeuValLysLeuAsnSerGlnAlaArgLeuSerSerMetValLys 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCCTCGT
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                                                                                                                                                                  IleSerProGlnAspCysThrLysValTyrLysAspLeuLeuGluAsnSe
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                                         ACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCT 641
                                                                            lSerGlyTrpGly.....
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Percent Identity:
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192

92 49 42 33

|||:::||| |GlyAlaProCysAlaArgGlySerHisProTrpGlnValAlaLeuLeuSe

GGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCCGCAGTGGGTGC

66

83 AspThrLeu...GlyAspArgArg.....AlaGlnArgIleLysAlaSe

CACAGTCTTGAGGCCGACCAAGAGCCAGGGGGGGCCAGATGGTGGAGGCCAG

euThrAlaAlaHisCysLysMetAsnGluTyTThrValHisLeuGlySer TGTCAGCCGCACACTGTTTCCAGAACTCCTACACCATCGGGCTGGGCCTG rGlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrpValL

CCTCTCCGTACGGCACCCAGAGTACAACAGACCCTTGCTCGCTAACGACC

rLysSerPheArgHisProGlyTyrSerThrGlnThrHisValAsnAspL

113

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alignment_block:
                                                                                                                                                                              alignment_scores:
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                                     Align seg 1/1 to: W05383 from: 1
                                                                        US-09-030-606-173 x W05383
                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
    W05383 standard; Protein;
                                                                                                                                                                                                                              conditions, esp. Alzheimer's disease

Claim 1: Page 44-45: 55pp; English.

Human amyloid precursor protein protease (W05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (T39783) obtd. Irom a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic (partic. AV-120 host cells. It is used to develop products for the design and testing of cpds. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease.

Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated {\sf develop}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1995; US-416257.
(ELIL ) LILLY & CO ELI.
Dixon EP, Johnstone EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens. W09631122-A1.
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Amyloid precursor
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1 GGCAGCCCG......CACTCGCAGCCCTGGCAGGCGGCACTGGTCAT 41
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                                                                                                                                                             Quality:
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rsor protein protease; Alzheimer's disease; diagnosis;
                                                                                                                        519.50
3.038
69.231
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                                                                                                                        42.915
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seq_name: A_Geneseq_36:W10694
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Antibody against neuropsin - used in the treatment of Alzheimer's disease and epilepsy (Claim 1; Page 7; 9pp; Japanese. W10694 is a recombinantly produced human neuropsin protein. The main invention relates to an antibody against the neuropsin protein, in particular a claimed fragment of the neuropsin protein (see W10695 and features table). The antibody can be used to treat neurodegenerative disorders such as Alzheimer's disease and epilepsy. Sequence 260 AA;
                                                                                                                             24-SEP-1996.
14-MAR-1995; 083154.
14-MAR-1995; JP-083154.
(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO WPI; 96-482259/48.
N-PSDB; T48519.
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                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                     Human recombinant neuropsin, used for antibody production. Antibody; Alzheimer's disease; neurodegenerative; epitope;
                                                                                                                                                                                                                                                                                                                                                                              W10694 standard; Protein; 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
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                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                          recombinant.
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TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGl
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antibody production"
                                                                                                                                                                                                                                                              Location/Qualifiers
95. .215
                                                                                                                                                                                                                                                 "claimed fragment
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alignment_scores

seq_documentation_block:
ID W12393 standard: Pr

Protein;

260

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seq_name: A_Geneseq_36:W12393
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Percent Similarity:
                                         246
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                                                                                                                                                          648 AAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTG
                                                                                                                                                                                                                                                                                                                        548 CTGCGCCGGCGGAGGCCAAGACCAGAAGGACTCCTGCAACGGTGACTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                     498 GAGGAGGTCTGCAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 TCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 GTTTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCC
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                                     |::::::||| ||||||:::|||||||:::
sArgTyrThrThrTrpIleLysLysThrMet
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                                                                               CAAATTCACTGAGTGGATAGAGAAAACCGTC 728
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                                                                                                                     SerAspProCysGlyLysProGluLysProGlyValTyrThrLysIleCy
                                                                                                                                                                                                lyGlyProLeuValCysAspGlyMetLeuGlnGlyIleThrSerTrpGly
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alignment_block:
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Claim 1; Page 6-7; 9pp; Japanese.

Chis is the amino acid sequence of a novel mouse protein designated neuropsin. The encoding gene was isolated from a mouse hippocampal conversation of the encoding gene was isolated from a mouse hippocampal conversation of the gene (clone B41; T63254). This fragment was amplified using primers T63252-3. The primers were synthesised based on the serine protease domain of nerve growth factor (NGF) gamma. The screen isolated positive clones, of which colone NP5 contained the longest insert (this sequence). The protein has a molecular weight of acund 26 kD.

It has 43% homology with EGF-BP, 41% with NGF-gamma; 39% with NGF-alpha; diagnosts and treatment of cerebral diseases.
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13-MAR-1996; 056367.
14-MAR-1995; JP-054584
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J08311099-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W12393;
15-MAY-1997
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WPI: 97-061812/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCACTCGCAGCCCTGGCAGGCGCACTGGTCATGGAAAACGAATTGTT
CTGGGGTCTGCCGGAACGGTGAGCTCACGGGTGTGTCTGCCCCTCTT
                                    GlnLeuAlaAsnLeuCysProLysValGlyGlnLysCysIleIleSerGl
                                                                           AGCATTGCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCCTCGTTTCTGG
                                                                                                                                                        TCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATC
                                                                                                                                                                                                                                     CCCAGAGTACAACAGACCCTTG
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                                                                                                                 eulleArgLeuGlnAsnSerAlaAsnLeuGlyAspLysValLysProVal
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71.311
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seq_documentation_block:
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Human serine protease; HGBAB90; pulmonary emphysema; pancreatitis; arthritis; multiple sclerosis; peridontal disease; cystic fibrosis; respiratory disease; thrombosis; cancer; cachexia; angina; glaucoma; inflammatory disorder; osteoporosis; cardiovascular disorder; hypertension; atherosclerosis disorder; cardiac infarction; stroke; asthma; psoriasis; chronic neurodegenerative disease; Alzheimer's; Parkinson's; Huntington's; demyelinating disease; Alzheimer's; parkinson's; hypertension; lans cataract formationgan transplant rejection; cataract; restenosis; muscular dystrophy renal failure; cerebral vasospasm; diabetic nephropathy.
                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1998;
21-APR-1998;
01-DEC-1997;
09-JUN-1997;
The present sequence represents a human serine protease (designated HGBAB90). HGBAB90 polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the HGBAB90 gene, and can diagnose diseases associated with HGBAB90 imbalance by determining HGBAB90 polypeptide expression levels. HGBAB90 polypeptides can be used to screen for agonists and antagonists, which can be used in treatment to activate (agonist) or inhibit (antagonist) HGBAB90 activity, in addition to direct administration of antisense sequences or soluble HGBAB90 polypeptides which competitively bind HGBAB90 ligands to prevent expression. Gene therapy may also be use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197
                                                                                                                                                                                                               New human serine protesse HGBAB90 polypeptide and polynucleotide useful as diagnostic reagents and for prevention and treatment of cancer, Alzheimer's disease and AIDS immune deficiency Claim 1; Page 13; 19pp; English.
                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM PLC.
BUTGESS NA, Clinkenbeard HE, Southan CD;
WPI; 99-047881/05.
N-PSDB; V84052.
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alignment_block:
US-09-030-606-173 x w87703
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sProCysTyrAsnSerSerAspValGluAspHisAsnHisAspLeuMetL
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                                                      CTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCCTGCAACGGTGACTCTG 597
                                                                                                      GlnLysLysCysGluAspAlaTyrProGlyGlnIleThrAspGlyMetVa
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alignment_block:

Percent Similarity:

Percent Identity:

Ratio:

US-09-030-606-173 x W45395

Align seg 1/1 to:

W45395

from:

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10 CACTCGCAGCCCTGGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTG

CTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTT HisSerGlnProTrpGlnValAlaValTyrSerHisGlyTrpAlaHisCy

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alignment_scores:
Quality:
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                                                                                                                    This polypeptide comprises human mature prostate-specific glandular kallikrein hK2. It is encoded by cDNA (see V06602) derived from human benign prostate hyperplasia (BPH) tissue RNA. The invention provides a diagnostic method comprising contacting antibodies that specifically bind to pro-hK2 (phK2, see W45396) or mature hK2 with a sample of physiological fluid from a human. The assay is based on the discovery that phK2 is detected in the supernatant of a prostate carcinoma cell line and that hK2 is present in human physiological fluid from prostate cancer cells. The method is useful for monitoring the treatment and/or prostate cancer in males that have BPH or a high grade prostatic neoplasia (HeCN) or whose family members have or had BPH, HPGN or a prostate cancer. Monitoring the presence and/or amount of hK2 complexes with plasma proteins may also be important in distinguishing between prostate cancer and BPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mature prostate specific glandular kallikrein hK2.
Prostate specific glandular kallikrein; hK2 protein; antigen;
prostate carcinoma; prostate cancer; benign prostatic hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnostic methods using antibodies which bind prostate antigens useful for, e.g. monitoring treatment or progression of prostate
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WO9802748-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
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15-JUL-1996; US-680868.
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233 leAlaAlaAsn 236
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                                           727 TCCAGGCCAGT 737
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| OAlaValTyrThrLysValValHisTyrArgLysTrpTleLysAspThrI 233
                                                                                                          AGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCG 726
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Title: .
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1265
1 GGCAGCCCGCACTCGCAGCC.....AGAGANGNGCAAAAAAAAA 1265
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1373.683 Million cell updates/sec
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S 17 7 7 8 8	HSBCL3S HSBCL3S AC006486 HSWUBND7 HSAPCC2G HUMAPOCZI HUMAPOCZ HSBCL3S2 AB012761 AF095743 E13202 D78203 D78203 HSUG28811	1135 1148 1148 1148 1148 1148 1148 1148 114	AF113141
AF015988 Homo sap1 195869 Sequence 2 AF055481 Homo sap1 G41906 SHCC-56840 A42048 Sequence 1 L33404 Human strat X59013 Rat mRNA fo U92372 Homo saplen X56744 P.platessa X822223 P.magellan1	Homo sapuman protioman apoluman apoluman apoluman apoluman apoluman apoluman apoluman protiomo sapien in s	135023 256 Sus 0019979 0078782 0780 Ho 079 Hum 079 Hum 93500 Ho 007392 00780 Ho 00780 Ho 0071712 0011712 0011712 0011712 0011712 0011712 0011712 0011712 0011712 0011712 0011712	141 Homo

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ALIGNMENTS

TITLE	REFERENCE AUTHORS	JOURNAL	TITLE	AUTHORS		ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 AF113140
Direct Submission	2 (bases 1 to 1347) Nelson,P.S., Gan,L., Ferguson,C., Moss,P., Gelinas,R., Hood,L. and	expression Proc. Natl. Acad. Sci. U.S.A. 96 (6), 3114-3119 (1999) 99179024	wauy, a. Molecular cloning and characterization of prostase, an androgen-regulated serine protease with prostate-restricted expression	L (Dases 1 to 1347) Nelson,P.S., Gan,L., Ferguson,C., Moss,P., Gelinas,R., Hood,L. and	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	numan. Homo sapiens		94512029 AF113140.1 GI:4512029	AF113140	Homo sapiens serine protease prostase mRNA, complete cds.	

Result No.

Query Score Match Length DB ID

SUMMARIES

972.4

76.9

1347

42 AF113140

Description

AF113140 Homo sapi

746

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polyA_site
BASE COUNT
ORIGIN
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           GCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTGTCTTTCGGAAAAGCCCCCGTGTGG
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                                                                      CATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCCTGCAACGGTGACTCTGGGGG
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Bothell, W
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ilarity 87.0%;
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/product="serine protease prostase"
/product="serine protease prostase"
/protein_id="sab21580.1"
/db_xref="piD:94512030"
/db_xref="0:4512030"
/db_xref="0:4512030"
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/translation="maraGnewGwFLGYLILGVAGSLVSGSCSQIINGEDCSPHSOPW
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VRHPEYNRPLLANDLMLIKLDESYSESDTIRSISIASQCPTAGNSCLVSGWGLLANGR
MPTVLQCVNVSVVSEEVCSKLYDPLYHPSMFCAGGGHDQKDSCNGDSGGPLICNGYLQ
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1. .765
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/db_xref="taxon:9606"
/chromosome="19"
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WA 98021, USA
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Pred. No. 3.5e-214;
0; Mismatches 22;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      Nelson, P.S.,
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Best Local Similarity 88.1%;
Matches 636; Conservative
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CCTCAGGCCCAGGAGTCCAGGCCCCCAGCCCCTCCTCCTCAAACCAAGGGTACAGATCC 885
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/protein_id="AAD21581.1"
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/db_xref="taxon:9606"
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Pred. No. 9.5e-118;
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Query Match
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37.5%;

Score 474.8; DB 42; Pred. No. 9.3e-100; 0; Mismatches 2;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification of novel human kallikrein-like genes 19q13.3-q13.4
Biochem. Biophys. Res. Commun. (1999) In press 2 (bases 1 to 4740)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                              Submitted (03-MAY-1999) School of Life Science, Queensland University of Technology, George Street, Brisbane, Queensland
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                            /gene="KLK4"
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/db_xref="taxon:9606"
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/product-"kallikrein
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                       'function="serine protease"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476;
                                                                                                                                                                                                                                     U76256
g2737920
U76256.1
2 (bases 1 to 1140)
Simmer, J.P., Fukkae, M., Tana
Margolis, H.C., Shimizu, M.,
Direct Submission
Submitted (24-OCT-1996) Pec
                                                                                         l (bases 1 to 1140)
Simmor,J.P., Fukae,M., Tanabe,T., Yamakoshi,Y., Uchida,T., )
Margolis,H.C., Shimizu,M., Hu,C.-C. and Bartlett,J.D.
Purification, Characterization and Cloning of Enamel Matrix
Proteinase 1
                                                                                                                                                                                                                                                                                               SSU76256
Sus scrofa
                                                                                                                                                                                           pig.
Sus scrofa
                                                                       Unpublished
                                                                                                                                                                 Eutheria;
                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                 complete
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                                                                                                                                           karyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
theria; Cetartiodactyla; Suina; Suidae; Sus.
(bases 1 to 1140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAD38019.1"
/db_xref="piD:95020096"
/db_xref="piD:95020096"
/translation="MATAGNPWGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPW
QAALVMENELFCSGYLVHPQWYLSAAHGFQNSYTIGLGLHSLEADQEPGSQMYEASLS
VRHPEYNRPLLANDLMLIKLDESVSESDTIRSISIASQCPTAGNSCLVSGWGLLANGR
MPTVLQCVNVSVVSESVCSKLYDPLYHPSMFCAGGGQDQKDSCNGDSGGPLICNGYLQ
GLVSFGKAPCGQVGVFGVYTNLCKFTEWIEKTVQAS"
                                                                                                                                                                                                                                                                                 cds.
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Pred. No. 9.4e-100;
0; Mismatches 2;
                              Tanabe,T., Y
,M., Hu,C.-C.
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x serine
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proteinase 1
                                             Yamakoshi,Y.,
                               and
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                               Bartlett
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Local Similarity 74.1%;
nes 640; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTTTCCAGAACTCCT 121
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                                                                                                                                                                                                                                                                                                         ACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAGAGCCAGGGAGCCAGATGG 181
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                                                                                                                                                                       TCATGCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCA 301
                                                                                                                                                                                                                                                                                                                                                                                                    ACACCATCGGGCTGGGTCTGCACAATCTTGAGCCCGAACAAGAACCCGGCAGCCAGATGA 357
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                                                                                                                                 TCATGCTCATCAAGTTGAAAGAATCGGTGTCGCTGTCTGACACCGTCCGGAACATCAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"the preprotein is cleaved following His30
activating the serine proteinase; the active protein has
an apparent molecular weight of 34 kDa and a derived
molecular weight of 24 kDa"
/product-"enamel matrix serine proteinase 1"
order(177. 179,549. 551)
/note-"disulfide bond"
order(234. 236,282. 284)
/note-"disulfide bond"
join(279. 281,414. 416,687. 689)
/note-"encodes catalytic triad"
405. 407
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b, TX 78284-7888, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="encodes potential glycosylation location; yields
blank cycle during protein sequencing"
order(408. .410,789. .791)
/note="disulfide bond"
order(510. .512,705. .707)
/note="disulfide bond"
order(675. .677,750. .752)
/note="disulfide bond"
a 366 c 295 g 234 t
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/product="enamel matrix serine proteinase 1 precursor"
/protein_id="anab94638.1"
/db_xref="piD:92737921"
/db_xref="piD:92737921"
/db_xref="GI:2737921"
/db_xref="
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/db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 452; DB 3;
Pred. No. 1.8e-94;
0; Mismatches 140;
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Mus musculus of complete cds.
AF019979
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AF019979.
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Health Science Center at San Antonio,
Antonio, TX 78284-7888, USA
                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                    Simmer,J.
                                                                                                                                                                                                                                                                                                              house mouse
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                                                 /organism="Mus musculus"
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/db_xref="taxon:10090"
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52. .126
52. .819
                                                                                                                                                                                                                                                                                                                                        Ļ
                        maturation"
                                                                                                                                    Location/Qualifiers
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           /note-"EMSP1"
                                    /function-"degradation
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nio, 7703 Floyd Curl Drive,
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SIQHPNENDPSFANDLMLIKLNESVIESNTIRSIPVATQCPTPGDTCLVSGWGQLKNG
KLPSLLGCVNLSVASEETCRLLYDPVYHLSMFCAGGGDQKDSCNGDSGGFIYCNRSL
QGLVSMGQGKCGQPGIPSVYTNLCKFTNWIQTIIQTN"
127. 144
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145..816
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Pred. No. 8.1e-62;
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 -ACTGACTACAAGGCCCACATGAA
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2E 1 (bases 1 to 35197)

2S Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,

Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,

Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J.,

Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J.,

Liu, S., Attix, C., Andreise, T., Trankheim, M., Anico-Reller, G.,

Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G.,

Kronmiller, B., Arellano, A., Wontgomery, M., Ow, D., Nolan, M.,

Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V.

Sequence analysis of an -700 kb region in 19q13.4 between D195268
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Submitted (05-OCT-1998) Joint Genome Institute,
National Laboratory, 7000 East Ave., Livermore,
Location/Qualifiers
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AC005782
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                                                              /note="BLASTX similarity to Q08509 (311. .346); match: 0.52, score: 3.3e-23; database searched: nr; EPIDERWAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >pir||539983 eps8 protein - mouse >gi|309217 (L21671) Eps8 [Mus" 155. .243
/note="predicted exon, frame: 0, quality: exce 251. .279
                                                                                                                                                                                     5HL2-B which carries chromosome."
                                                                                                                                                                                                                            /note="Cosmid library LL19NC03 was constructed at LLNL
from flow-sorted chromosomes from human-hamster hybrid
                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                             /map="19q13.4 between D19S268
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                                                                                                                                                                                                                                                                                                                                                        chromosome="19"
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                       program: grail2exons_human_1.3,
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	misc_feature	misc_feature		misc_feature	repeat_region	repeat_region	_region	repeat region			misc_feature	repeat_region				miscTreature	fortur			m1sc_reature	•	misc_feature	misc_feature		misc_teature	
frame: 1, quality: excellent, score: 90.000DDS similarity to :-(41244215) R34158 yh83h09.s1 Homo sapiens cDNA clone 136385 3' similar to Sp:S39983 S39983 EPS8 PROTEIN; (272364); 94% identity(41244136) H13945 yj08d11.s1 Homo sapiens cDNA clone 148149 3' similar to Sp:S39983 S39983 EPS8 PROTEIN; (324336); 100% identity."	CDNA clone 136385 3' Similar to Sp.539983 S39983 EPS8 PROTEIN: (224271); 100% identity." 124425 /note="predicted exon, program: grail2exons_human_1.3,	PROTEIN: (1911.1323) 55% identity: "500 E500 E500 E500 E500 E500 E500 E500	Similarity to overlapping ESTs:~(3904. 3988) R80263 y196h06.s1 Homo sapiens cDNA clone 147131 3'; (216. 300); 96% identity.~~(3904. 4036) H13945 y198dd11.s1 Homo sapiens CDNA clone 148140 3', similar to SB.S30083 S30083 BBS8	39044036 /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 99.000DDS	/rpt_family-"MIR"	/FPC_Idmily"MIK" complement(3241, 3527) /rot family="Alico"	/rpt_family="MSR1" 31603240	Homo sapiens cDNA clone 148149 3' similar to SP: 339983 S39983 EPS8 PROTEIN; (162190); 93% identity."	identity R80263 y196h06.sl homo sapiens cDNA clone 147131 3': (187. 215): 97% identity H13945 v108411 sl	yh83h09.s1 Homo sapiens cDNA clone 136385 3' similar to Sp.s39983 Sagara EPSR PERCEPTN. /195 2231. 078	1679. 1707	<pre>complement(16211652) /rpt_family="GC_rich"</pre>	148149 3' similar to SP:S39983 S39983 EPS8 PROTEIN; (21161); 94% identity."	Homo sapiens cDNA clone 147131 3'; (46186); 948 Identity.~~H13945 v108d11.sl Homo sapiens cDNA clone	frame: 1, quality: excellent, score: 75,000DDS similarity to overlapping ESTs:-R34158 yh83h09.s1 Homo sapiens cDNA clone 136385 3' similar to SP:S39983 S39983 EPS8 PROTEIN: 756 1343: 348 identityR80763 v196h06 s1	/note-"predicted exon, program: grail2exons_human_1.3,	complement(11451258) /rpt_family="FLAM_C"	SF:S39983 S39983 EFS8 FKOTELN; (1S); 100% identity(621665) R80263 y196606.s; Homo sapiens cDNA clone 147131 3'; (145); 100% identity."	frame: 0, quality: excellent, score: 100.000DDS similarity to overlapping ESTs:-(611665) R34158 yh83h09.s1 Homo sapiens CDNA clone 136385 3, similar to	<pre>/note="predicted exon, program: grail2exons_human_1.3,</pre>	/note="BLASTX similarity to Q08509 (368. 415); match: 0.52, score: 3.3e-23; database searched: nr; EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >pir S39983 eps8 protein - mouse >gi 309217 (L21671) Eps8 [Mus"	frame: 1, quality: excellent, score: 100.000" 517. 660	<pre>338. 412 /note="predicted exon, program: grail2exons_human_1.3,</pre>	GROWTH FACTOR RECEPTOR KINASE SUBSTRACE FIRS 911 1839983 eps8 protein - mouse >91 309217 (L21671) Eps8 [Mus"	338430 /note="BLASTX similarity to Q08509 (343373); match:	/rpt_family="GC_rich"
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_featur	misc_feature	misc_feature	misc_feature	repeat_region	misc_feature	misc_feature	misc_feature		misc_feature	repeat_region	repeat_region	repeat_region		misc_feature	misc_feature			misc_feature		misc_feature		misc_feature	repeat_region	mrsc_reardre		misc_feature
ი ωთი	11 aune: 1. quality: excellent, score 19.000(10928. 1.1996) DDS similarity to R35625 yg66g06.r1 Homo sapiens cDNA clone 38310 5'; (319341); 78% identity." complement(1107911139)	complement(10810. 10931) /note="predicted exon, program: grail2exons_human_1.3, /note="predicted exon, program: grail2exons_human_1.3,	<pre>/rpt_family="GC_rich" complement(1068510725) /note="predicted exon, program: grail2exons_human_1.3,</pre>	<pre>/note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 100.000" complement(1058010651)</pre>	<pre>//nove= predicted exon, program: grailzexons_numan_i.s, frame: 0, quality: excellent, score: 100.000" complement(1028510389)</pre>	frame: 1, quality: excellent, score: 92.000" complement(9677. 9763)	- = -	clone balance of the second se	O T23821 SEC1081 HOMO	\running -	7429. 8057	<pre>complement(68676897) /rpt family="GC rich"</pre>	colon 9."	7557. 58525983 700fe="HIASTN similarity to D25793 (1132): match: 0.98.	<pre>complement(56915961) /note="DDS similarity to R34157 yh83h09.r1 Homo sapiens cDNA clone 136385 5'. Score: 513 Identity: 268/270 /008 "</pre>	sapiens CDNA Clone IMAGE:1/13349 3', mxNA sequence [Homo sapiens]"	0.99, score: 5.0e-144; database searched: month.na; 0.99, score: 5.0e-144; database searched: 5.0	PROTEIN; (2351); 99% Identity." complement(56195988) /nofe="milestu similarity to All26400 (11380): match:	frame: 1, quality: excellent, score: 89.000DDS similarity to:-(5591 .5825) H13944 yj08d11.r1 Homo sapiens CDNA clone 148149 5' similar to SP:S39983 S39983 EPS8	<pre>55915677 /note="predicted exon, program: grail2exons_human_1.3,</pre>	frame: 2, quality: excellent, score: 93.000~-DDS similarity to:-(53675498) H13944 yj08d11.r1 Homo sapiens cDNA clone 148149 5' similar to SP:S39983 S39983 EPS8 PROTEIN; (368236); 93% identity.	53665498 // State of the control	<pre>complement(48174878) /rpt_family="GC_rich"</pre>	<pre>///</pre>	<pre>/note="predicted exon, program: grail2exons_human_1.3, frame: 2, quality: excellent, score: 95.000" /777</pre>	44554581

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JOURNAL REFERENCE
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REFERENCE
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AUTHORS
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ORGANISM
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Best Local Sim
Matches 281;
                                                                      AUTHORS
TITLE
JOURNAL
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TITLE
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Direct Submission
Submitted (22-DEC-1998) Barton P.J.R., Cardiothoracic Surgery,
Mational Heart & Lung Institute, Imperial College of Science, Tech. &
Med., Dovehouse Street, London SW3 6LY, UK
On Dec 29, 1998 this sequence version replaced g1:1524065.
                                                                                                                                                Direct Submission.

Direct Submission.

Submitted (15-AUG-1995) P.K. Bhavsar, Cardiothoracic Surgery,

Submitted (15-AUG-1995) P.K. Bhavsar, Cardiothoracic Surgery,

National Heart & Lung Institute, Imperial College of Science, Tech. &

Novehouse Street, London SW3 6LY, UK
                                                                                                                                                                                                                                                                                                    Barton, P.J.R., Cullen, M.E., Townsend, P.J., Brand, N.J., Mullen, A.J., Norman, D.A.M., Bhavsar, P.K. and Yacoub, M.H. Close physical linkage of human troponin genes: organization, sequence, and expression of the locus encoding cardiac troponin I and slow skeletal troponin T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6592)

Bhavsar, P.K., Brand, N.J., Yacoub, M.H. and Barton, P.J.R.
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(bases 1 to 6592)
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sapiens INNI3 ge
780 X90781 X90782
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83.1%;
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                                                                                                                                                  /gene="TNNI3"
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6442
                                               6526..6592
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6568..6573
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               /note="putative" 1836 c 2048
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/translation="MADGSSDAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISAS
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RVDKVDEERYDIEAKVTKNITEIADLTQKIFDLRGKEKRFTLRRVRISADAMMQALLG
RARKESLDLRAHLKQVKKEDTEKENREVGDWRKNIDALSGMEGRKKKFES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Join(1250. .1260,1532. .1544,1706. .1789,2195. .
2507. .2638,4009. .4098,4633. .4809,6442. .6525)
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2507. .2638,4009.
/gene="TNNI3"
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                                                                                                                                                                                                                                   'gene-"TNNI3"
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'gene="TNNI3"
                                                                                                                                                                                                                                                                                                                                       'gene="TNNI3"
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'gene="TNNI3"
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Similarity

15.18;

Score 190.8; DB Pred. No. 1.9e-34 0; Mismatches 7

10;

6592; 12;

Indels Length

Gaps

5

Conservative

/partial /gene="XRCC1" /note="exon 3; G00-120-737" /492225080 /partial /gene="XRCC1"		/partial /gene="xRCC1" /note="exon 1; G00-120-737" exon 47244816	/gene**XRCC1* exon 42684318	/tissue_lib="LL19NC02-F2" /map="19q13-2" gene 4268.	/cell_line="NV5H19-5B" /cell_type="lymphocyte" /dev_stage="adult" /tissue_type="blood"	FEATURES Location/Qualifiers source 137785 /organism="Homo sapiens" //th yref="tayon.ofof"	Genomic sequence comparison of the gene regions L Genomics (1995) In press	Euka Euthe 1 (l Lames	VERSION L34079.1 GI:642116 KEYWORDS Alu repeat; DNA repair protein; tandem satellite array. SOURCE Homo sapiens (tissue library: LL19NC02-F2) adult blood DNA. ORGANISM Homo sapiens	LOCUS HUMXRCC1G 37785 bp DNA PRI 30-JAN-1995 DEFINITION Human XRCC1 DNA repair gene, genomic. ACCESSION L34079 NID G642116	SULT 9	QY 1136 CCACCTAGATTTTCCCT 1152	QY 1076 TTCCCCAGACCCAGAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAATG 1135	QY 1016 GGGTTGAGGCCCCCAACCCCTCCTTCAGAGTCAGAAGGTCCAAGCCCCCAACCCCTCG 1075	QY 956 GCCCTCCTCCNTCAGACCCAGGAGTCCAGACCCCCAGCCCCTCCCTCAGACCCAG 1015	QY 903 AGACCCAGGAGTCCAGACCCCCAGCCCCTCCTCAGACCCCAGGAGTCCA 955	QY 843 CAGGCCCCCAGCCCTCCTCCAAACCAAGGGTACAGATCCCCAGCCCCTCCTCCTC 902	Oy 783 CCTGCGGAAGGAATICAGGAATATCTGTTCCCAGCCCCTCCTCCCTCAGGCCCAGGAGTC 842
Query Match 15.0%; Score 190.2; DB 9; Length 37785; Best Local Similarity 74.6%; Pred. No. 2.4e-34; Matches 302; Conservative 0; Mismatches 91; Indels 12; Gaps 5;	/note="exon 17; G00-120-737" BASE COUNT 8717 a 9329 c 9806 g 9929 t 4 others ORIGIN	/note="exon 16; G00-120-737" exon 36082, .36195 /partial /gene="XRCC1"	1 XRCC1"	/gene="XRCC1" /note="exon 15; G00-120-737" exon 389935975	/partial /gene="XRCC1" /note="exon 14; G00-120-737" exon 3535335443 /partial	/gene="XRCC1" /note="exon 13; G00-120-737" exon 33629. 33768	/note="human chromosome 19-specific tandem repeat, pE670" exon 3348033534 /partial	/gene="xrcc1" /gene="xrcc1" /note="exon 12; G00-120-737" satellite complement(3300133360) /partial /gene="xrcc1"	/gene="XRCC1" /gene="XRCC1" /note="exon 11; G00-120-737" exon . 32859. 32991 /partial	/partial /gene="xRCC1" /note="exon 10; G00-120-737" exon 32609. 32702	/gene="XRCC1" /gene="XRCC1" /note="exon 9; G00-120-737" exon 28039 28155	/gene="XRCC1" /note="human chromosome 19-specific tandem repeat, pE670" exon 27451 .27709	/gene="axcc1" /note="exon 8; 600-120-737" satellite complement(27008. 27410) /partial	/gene="XRCC1" /note="exon 7; G00-120-737" exon 2681826929 /partial	yene="ARCC1" /note="human chromosome 19-specific tandem repeat, pE670" exon 26635. 26744 /partial	/gene="XRCC1" /note="exon 6; G00-120-737" satellite complement(2634226484) /partial	/gene="AKCC1" /note="exon 5; G00-120-737" exon 2621426325 /partial	/note="exon 4; G00-120-737" exon 2604326117 /partial

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978
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                                         CCCTCCTCCCTCAAACCAAGG-GTACAGATCCCCAGGCCCTCCTCCCTCAGACCCAGGAG 913
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                    CNTCAGACCCAGGAGTCCAGACCCCCCAGCCCCTCCTCCTCAGACCCAGGGGTTGAGGC 1025
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I34189
                                                                                                                                                                                                                                                                                                               Methods and products for the synthesis of oligosaccharide structures on glycoproteins, glycolipids, or as free molecules, for the isolation of cloned genetic sequences that determine the
                                                                                                                                                                                                                                                                     Patent: US 5595900-A 5 21-JAN-1997;
Location/Qualifiers
1. 8174
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2229 c 2322 g
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Pred. No. 5.1e-33;
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K03500.1 GI:337672
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Human 37 bp minisatellite repeats,
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                                                                                                                                                                                                                                               58
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="COS 4C"
/cell_line="JY"
1. .37
                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                           /note="sat rpt copy C" 114. .151
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152. .
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CCCCCCAGCCCTCCTCAGACCCAGGGGTTGAGGCCCCCAACCCCTCCTTCAG 1046
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                                                                                                                                                                                                      CCCTCAGACCCAGGAGT------CCAGCCCCTCCTCCNTCAGACCCAGGAGTCCAGA 986
                                             AGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAGACCCAGAGGTNNAG-GTCCCAGC 1105
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ACCCAGGAGTCCAGACCCCCAGCCCCTCCTCCTCAGACCCAGGAGTCCAGACCCCCAGC
                                                                                                   CCCCCCAGCCCCTCCTCCAGACTCATGAGTCCAGACCCCCAGCCCCTCCTCCTCAG
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 281)
Das, H.K., Jackson, C.L., Miller, D.A., Leff, T. and Breslow,
The human apolipoprotein C-II gene sequence contains a no
chromosome 19-specific minisatellite in its third intron
J. Biol. Chem. 262 (10), 4787-4793 (1987)
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                                                        381
                                                                                                                                 Local Similarity 76.9 hes 283; Conservative
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                  CCCTCCTCCTCAAACCAAGG-GTACAGATCCCCAGCCCCTCCTCCTCAGACCCAGGAG
                                                        ACTTAGGAGTCCAGGCTCCCGGCCCTCCTCCCTCAGACCCAGGAGTCCAAGCCCCCTGC
                                                                          ATTCAGGAATATCTGTTCCCAGCCCCTCCTCCCTCAGGCCCCAGGAGTCCAGGCCCCAGC 854
Larsen, R.D., Ernst, L.K., Nair, R.P. and Lowe, J.B. Molecular cloning, sequence, and expression of a human GDP-L-fucose: beta -D-galactoside 2-alpha-L-fucosyltransferase that can form the H blood group antigen Proc. Natl. Acad. Sci. U.S.A. 87 (17), 6674-6678 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-SEP-1996) to the DDBJ/EMBL/GenBank databases. Hiroshi Kimura, Kurume University, School of Medicine, Department of Legal Medicine; 67 Asahimachi, Kurume, Fukuoka 830, Japan (E-mail:hkimura@kurume.ktarn.or.jp, Tel:0942-31-7554, Fax:0942-31-7700)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure and expression of H-type GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase gene (FUT1). Two transcription start sites and alternative splicing generate several forms of FUT1 mRNA J. Biol. Chem. 272 (11), 7501-7505 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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D87943.1 GI:1842173
EVTI; alpha (1, 2) fucosyltransferase.
Homo sapiens peripheral leukocytes DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          para-Bombay individuals
Proc. Natl. Acad. Sci. U.S.A. 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular basis for H blood group deficiency in Bombay (Oh) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kelly, R.J., Ernst, L.K., Larsen, R.D., Bryant, J.G., Robinson, J.S. and
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                                                                                                                                                                                                                                                                                                            /gene="FUT1"
1. .1665
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                          /gene-"FUT1"
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="peripheral leukocytes"
1. .1665
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                                                                                                                                                   13.4%;
76.9%;
                                                                                                                               Score 169; DB 9; Length 1665;
Pred. No. 2.1e-29;
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                                                                                                                                                                                                                                                                                          Submitted (06-AUG-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from g centromere to telomere. BAC 338531 (CIT-HSP 490g23) is adjacent to cosmid F24498 to the left and overlaps BAC 52850 (CIT-HSP 6117) to the right by approximately 35 kb. Accession does not represent the sequence of the entire BAC clone insert at this time. Additional chr 19 map and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W., Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J., Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Montgomery, M., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of a 2.5 Mb region in 19q13.2 containing a clustered CEA/PSG gene family
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AC005392.1 GI:3399669
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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/note="LLNL clone name:
complement(566. .1150)
/rpt_family="MER67C"
                                                                                     /map="19q13.2 between /clone_11b="CIT-HSP"
                                                                                                                                                   /clone="490g23"
                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                  /tissue_type="sperm"
                                                                                                                              /chromosome="
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/rpt_family="Alusp"
/rpt_family="Mer65_internal"
/rpt_family="Mer65_intern
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/rpt_family="Alusg"
complement(14308...14692)
/rpt_family="MER57_internal"
14855...15152
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/rpt_family="AluSg"
complement(13074..13218)
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/rpt_family="Aluy"

complement(7329..7457)

/rpt_family="MER4_internal"

7478..7839
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complement(8259. .9153)
/rpt_family="LIPA2"
9684. .9975
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/rpt_family="(TA)n"
7937...8213
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/rpt_family="L1"
complement(6416..6557)
/rpt_family="L1M4"
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complement/13056
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12692. .12869
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12399.
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12362
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/rpt_family="MIR"
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11171. .11311
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/rpt_family="Alu"
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4581. :4774
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4498. .4578
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4129. .4417
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complement(23264. .23758)
complement(23264. .23758)
score: 3.9e-158; database searched: nr; pregnancy-specific beta-1-glycoprotein 11 form w precursor - human"
complement(3506. .2368)
note="DDS similarity to W49630 zc42h12.rl Soares senescent fibroblasts NbHSF Homo saplens cDNA clone 325031
5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1
GLYCOPROTEIN C PRECURSOR (HUMAN); (1. .183); 99% identity."
complement(23507. .23758)
note="BLASTN similarity to (331. .414); match: 0.86, score: 5.7e-104; database searched: nr; pregnancy-specific beta-1-glycoprotein 11 form r precursor - human"
complement(23561. .23760)
note="BLASTN similarity to T39371 (75. .274); match: 1, score: 1.7e-95; database searched: est; ya05b01.rl Homo sapiens cDNA clone 6053 5' similar to SP:A33514 A33514
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR -"
complement(23685. .23760)
note="BLASTN similarity to T39410 (75. .150); match: 1, score: 7.0e-47; database searched: est; ya05f02.r3 Homo sapiens cDNA clone 60603 5' contains Alu repetitive element."
                                                     complement (24158.
                                               sapiens cDNA clone
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20467. .22597
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19981. .20294
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/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                     complement(23704.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="MIR"
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complement(18346. .18385)
/note="DDS similarity to W43007 zc24g09.s1 Soares
senescent fibroblasts NbHSF Homo sapiens cDAR clone 323296
3' similar to gb:M20882 PREGNANCY-SPECIFIC BETA-1
GLYCOPPOTEIN E PRECURSOR (HUMAN); (441. .402); 100%
identity."
complement(18346. .18429)
/note="DDS similarity to W49630 zc42h12.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 5' similar to 95:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN); (184. .267); 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREGUNNCY SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN); (268.524); 99% identity." complement(1667.16961)
/rpt_family="Alux"
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Db 201638 CAGGAGTCCAGGCCCCCAGTCCCTCCTCCTCAGACCCCAGGAGTCCAG-GCCCCAGTGC
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Submitted (22-DEC-1998) Barton P.J.R., Cardiothoracic Surgery, National Heart & Lung Institute, Imperial College of Science, Tech. & Med., Dovehouse Street, London SW3 6LY, UK
On Dec 29, 1998 this sequence version replaced gi:1524065.
This sequence is directly followed by the slow skeletal troponin T gene (AC AJ011712, AJ011713)
                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 6592)
Barton, P.J.R., Cullen, M.E., Townsend, P.J., Brand, N.J., Mullen Norman, D.A.M., Bhavsar, P.K. and Yacoub, M.H.
Close physical linkage of human troponin genes: organization, sequence, and expression of the locus encoding cardiac tropon and slow skeletal troponin T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6592)

Bhavsar, P.K., Brand, N.J., Yacoub, M.H. and Barton, P.J.R.
Isolation and characterization of the human cardiac troponin I gene
                                                                                                                                                                                                  Submitted (15-AUG-1995) P.K. Bhavsar, Cardiothoracic Surgery, National Heart & Lung Institute, Imperial College of Science, Tech. & Med., Dovehouse Street, London SW3 6LY, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X90780.1 GI:4071059 cardiac troponin I; TNNI3 gene.
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X90780 X90781 X90782
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                                                                                                                                                              Revised by [3]
4 (bases 1 to 6592)
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Pred. No. 3.9
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                                                          Conservative
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1107..1249
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6568. .6573
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RKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPLELAGIGFAELQDLCRQLHA
RVDKVDEERYDIEAKVTKNITEIADLTQKIFDLRGKFKRPTLRRVRISADamMQALLG
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/db_xref="pID:e196058"
/db_xref="pID:91524066"
/db_xref="0I:1524066"
/db_xref="SWISS-PROT:P19429"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                  gene-"TNNI3"
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/number=7
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/number=6
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/product="cardiac
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507. .2638,4009. .4098,4633. .4809,6442. .6525)
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'gene="TNNI3"
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.2638,4009. .4098,4633. .4809,6442. .6592)
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Pred. No. 1.3e-28;
0; Mismatches 97;
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2301.1"
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KEYWORDS SOURCE ORGANISM

Homo sapiens

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ACCESSION

RESULT 14 HSCTPI1T5/c

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Query Match Best Local Sim Matches 244;

Similarity

Conservative

misc_feature

REFERENCE AUTHORS

TITLE

TNNI3

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AUTHORS TITLE

Barton, P.J.R. Direct Submission

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Unpublished

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Direct Submission 3havsar,P.K.

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JOURNAL MEDLINE

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                                                                                                                                                                                                                                                                 human Eerythroid lineage
Unpublished (1998)
On Jun 20, 1998 this sequence version
Sequence updated (16-Jun-1998).
                                                                                                                                                                                                                                                                                                                          Koda,Y., Soejima,M. and Kimura,H. Changing transcription start sites in H type a(1,2)fucosyltransferase gene (FUT1) during a
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-AUG-1997) to the DDBJ/EMBL/GenBank databases. Yoshiro Koda, Kurume University, School of Medicine, Department of Forensic Medicine, Asahimachi 67, Kurume, Fukuoka 830, Japan (E-mail:ykoda@med.kurume-u.ac.jp, Tel:0942-31-7554,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB006136.1 GI:3242453
FUT1: alpha (1, 2) fucosyltransferase.
Homo sapiens peripheral leukocytes DNA.
Homo sapiens
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1 (bases 1 to 4033)
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4

Search completed: September 28, 1999, 12:24:11 Job time: 5131 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic . nucleic search, using sw model

Run on: September 28, 1999, 12:27:24; Search time 289.74 Seconds (without alignments) 1092.334 Million cell updates/sec

Perfect score: Sequence: Title:

Scoring table: Searched:

IDENTITY_NUC

US-09-030-606-173
1265
1 GGCAGCCCGCACTCGCAGCC.....AGAGANGNGCAAAAAAAAAA 1265

Database : N_Geneseq_36:*

311585 seqs, 125096042 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Dillon DC, Xu J;
WPI; 98-609886/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer Claim 3; Page 105-106; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic poof a prostate tumour protein. The encoded immunogen, or the DNA ican be used as a vaccine for the treatment of prostate cancer. The was identified by analysis of a subtracted cDNA library obtained subtracting a prostate tumour cDNA expression library with a norm tissue cDNA library.

Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T;
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WPI; 98:
P-PSDB;
                             Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers Claim 1; Page 112; 141pp; English.

This sequence represents a human prostate tumour specific gene, and car be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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WPI; 98-609886/51.
P-PSDB; W71871.
                                                                                                                                                                                                                          Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 104; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic port. of a prostate tumour protein. The encoded immunogen, or the DNA its can be used as a vaccine for the treatment of prostate cancer. The laws identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.

Sequence 1248 BP; 288 A; 424 C; 303 G; 228 T;
                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequence of prostate tumour clone P703 splice variant Prostate; cancer; tumour; vaccine; immunogen; clone; ss. Homo sapiens.
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27-AUG-1998: U03690.
25-FEB-1998: US-904809.
25-FEB-1997: US-806596.
01-AUG-1997: US-904809.
(CORI-) CORIXA CORP.
D1110n DC, Xu J;
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08-DEC-1998 (f1)
Prostate tumour s
Prostate tumour s
therapy; ss.
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Claim 1; Page 115; 141pp; English.

This sequence represents a human prostate tumour specific gene, and car be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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Homo sapiens.
W0983703-A2.
27-AUG-1998; U03492.
25-FEB-1998; U5-020956.
25-FEB-1997; U5-806099.
01-AUG-1997; U5-904804.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WFI; 98-609886/51.
P-PSDB, W71782.
Polypeptides comprising immunogenic pounds in a vaccine for the treatment of Claim 3; Page 107; 130pp; English.
The present sequence is a new DNA whic of a prostate tumour protein. The enco
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V61252;
06-JAN-1999 (first entry)
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26-MAR-1998.
05-SEP-1997; U15627.
21-JUL-1997; US-897340.
17-SEP-1996; US-715032.
(MILL-) MILLENNIUM PHARM I
EIRANGA PR. Gimeno CJ;
WPI; 98-217246/19.
P-PSDB; W59129.
                                                                                Claim 10; Fig 1; 120pp; English.

The sequence is that of the Tub Interactor gene hTI-1 which codes for a putative serine protease. TI genes function in biochemical pathways involved in weight control and related disorders. The products can be used for treating weight disorders, e.g. obesity, cachexia or anorexia nervosa, or a related disorder such as diabetes. The products can also be used to modulate cell cycle progression and apoptosis. They can be used for treating neurodegenerative diseases.
drug scre
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens Tub Interactor (hTI-1) gene. serine protease; tub interactor; treatment; obesity; cachexia; anorexia nervosa; diabetes; cachexia; apoptosis; neurodegenerative disease; Alzheimer's disease; drug screening; parkinson's disease; Huntington's chorea; detection; diagnosis; amylotrophic lateral sclerosis; spinocerebellar degeneration; si
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                                        which are characterised by apoptosis, including Alzheimer's disease, Parkinson's disease, Huntington's chorea, amylotrophic lateral sclerosis or spinocereballar degenerations. The
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Query Match
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                                                      AGCCCTCCTCCNTCAGACCCAGGAGTCCAGACCCCCAGCCCTCCTCCAGACCCAGACCCCAGGCCCTCCTCAGACCCAGGACCCCAGGCCCTCCTCAGACCCA
                                                                                                       CCTCCCTCAGACCCAGGAGTCCAGACCCCCCAGCCCTCCTCAGACCCAGGAGTCC
                                                                                                                                                                       TGCTGGCGAACGGTGAGCTCACGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCC 415
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                  CCTCCCTCAGACCCAGGAGTCCAGACCCCCCAGCCCCTCCTCAGACCCAGGAGTCC
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Query Match
Best Local Similarity
Matches 737; Conser
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(INCY-) INCYTE PHARM INC.
Bandman O, Goli SK;
WPI; 98-286933/25.
P-PSDB; W60592.
                                                                                                                                                                                                                                                                                                                                                      W09820117-A1.
14-MAY-1998.
31-OCT-1997; U
05-NOV-1996; U
                                                                   Claim 5; Fig 1A-C; 68pp; English.

This DNA encodes a human prostate-specific kallikrein (HPSK). A host cell containing an expression vector comprising the HPSK nucleic acid sequence can be used to produce the protein recombinantly. The HPSK products can be used for the diagnosis of conditions or diseases associated with expression of HPSK such as prostate carcinoma and benign prostate expression of the such as prostate carcinoma and benign prostate hyperplasia. Agonists and antagonists which specifically bind to HPSK and modulate its activity can be used for the preparation of treatment of such conditions or diseases. The products can also be used for detection and drug screening, especially for the detection of prostate-specific kallikrein (PSK).

Sequence 871 BP; 166 A; 260 C; 258 G; 184 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V37495 standard; DNA; 871 BP.
V37495;
07-SEP-1998 (first entry)
Human prostate-specific kallikrein (HPSK) encoding DNA.
Prostate-specific kallikrein; HPSK; prostate carcinoma;
benign prostate hyperplasia; diagnosis; drug screening;
Homo sapiens.
Location/Qualifiers
CDS
31..777
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Claim 5; Fi
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nilarity 89.0%;
Conservative
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/transl_except- (pos:412. .414,
/transl_except- (pos:424. .426,
/product- "HPSK protein"
/note- "Xaa - unknown"
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Score 641; DE Pred. No. 3.96 0; Mismatches
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prostate tumour specific ger
Prostate tumour specific ger
therapy; ss.
Homo sapiens.
W09837418-A2.
27-AUG-1998; U03690.
25-FEB-1998; US-904809.
09-FEB-1997; US-904809.
01-AUG-1997; US-904809.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI: 98-480805/41.
Novel human prostate
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Best Loc
Matches
                 Prostate; cancer; tumour; vi
Homo sapiens.
WO9837033-A2.
27-AUG-1998.
U03492.
09-FEB-1998; U03492.
09-FEB-1997; US-806099.
25-FEB-1997; US-904804.
(CORI-) CORIXA CORP.
D1110n DC, XU J;
D1110n DC, XU J;
D1110n DC, XU J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for detecting and treating prostate cancers
Claim 1; Page 114; 141pp; English.
This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
                                                                                                                                                                                                                                                          V61251 standard; cDNA; 145
V61251;
06-JAN-1999 (first entry)
cDNA sequence of prostate
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505 CAACG
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27-AUG-1998.
25-FEB-1998; US-904809.
09-FEB-1997; US-806596.
01-AUG-1997; US-904809.
(CORI-) CORIXA CORP.
D1110n DC, Xu J;
WPI; 98-480805/41.
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The present sequence is a new DNA which encodes an immunogenic po of a prostate tumour protein. The encoded immunogen, or the DNA i can be used as a vaccine for the treatment of prostate cancer. The was identified by analysis of a subtracted cDNA library obtained subtracting a prostate tumour cDNA expression library with a norm tissue cDNA library.

Sequence 1459 BP; 427 A; 328 C; 406 G; 295 T;
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Prostate tumour specific gene clone DE14
Prostate tumour specific gene; human; pro-
therapy: ss
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Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers

Claim 1; Page 116-117; 141pp; English.

This sequence represents a human prostate tumour specific gene, and car be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers.
Polypeptides comprising immunogenic portions of prostate proteins - used in a vaccine for the treatment of prostate cancer Claim 3; Page 108-109; 130pp; English.

The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             V61253;
V61253;
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X41114 standard; cDNA; 402 B

X41114;
17-JUN-1999 (first entry)
17-JUN-1999 (first entry)
New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue Claim 1; Page 205; 824pp; English.

X41094 to X41347 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in X12261 to X12514, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, chemotactic/
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WPI; 99-153778/13.
P-PSDB; Y12281.
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Human; secreted protein; EST; expressed sequence tag; diagnosis;
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upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopolesis regulation; tissue growth regulation;
reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
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AC Q14
COS HOMO
CH Key
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Best Loc
Matches
Isolation of gene conveying post-translational characteristic e.g. the presence of soluble or membrane bound oligo or polysaccharide or glycosyltransferase.

Disclosure; Fig 3; 155pp; English.

The DNA encodes a protein sequence capable of functioning as a GDP- Fuc:[beta-D-Gal alpha(1,2)- fucosyltransferase. The sequence coded by nucleotides 4782 - 5780 represents the functional protein. The enzyme produced by the DNA sequence can be used in enzymatic
                                                                                                                                                                                                                                                                                         WO9112340-A.
22-AUG-1991.
14-FEB-1991;
14-FEB-1990;
14-FEB-1990;
12-DEC-1990;
(UNMI) UNIV
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ligand activity, anti-inflammatory activity, tumour inhibition activity
or other activities. The products can be used in forensic, gene therapy
and chromosome mapping procedures. The sequences can also be used for
obtaining corresponding promoter sequences. The nucleic acids encoding
the signal peptide can be used for directing extracellular secretion of
a polypeptide or the insertion of a polypeptide into a membrane, or
importing a polypeptide into a cell.
sequence 402 BP; 80 A; 125 C; 121 G; 75 T;
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Q13332;
Q1-NOV-1991 (f1
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                                                                                                                                                                                                                  P-PSDB; R13751
                                                                                                                                                                                                                                          Lowe JB;.
WPI; 91-267151/36.
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US-479858.
US-627621.
US-62763N.
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3-75;
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Best Local Sim
Matches 272;
                                                                       Ouery Match
Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-1994,
20-JUL-1993; U06703,
20-JUL-1992; US-914281,
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                              DNA fragment encoding a glycosyltransferase - can be used for in vitro reactions to modify cell surface oligosaccharide(s) e.g. blood gp. determinants, to protect against transplant rejection Disclosure; Fig 3; 249pp; English.

The sequence is that encoding human glycosyl transferase. The enzyme produced by the DNA may be non glycosylated. This prevents premature loss of enzyme activity. It can also be used in in vitro reactions to modify cell surface oligosaccharide mols. e.g. blood group determinants. See also Q56905-12.

Sequence 8174 BP; 1628 A; 2228 C; 2322 G; 1996 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a glycosyltransferase. Glycosyltransferase; fucosyltransferase; surface; oligosaccharide; ss.
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Sequence 8174 BP; 1628 A; 2229 C; 2322 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lowe JB;
WPI; 94-048874/06.
P-PSDB; R45936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q56908 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1025
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72; Conservative
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                               14.6%;
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                                                                       Score 184.6; DB 1;
Pred. No. 6.7e-36;
0; Mismatches 64;
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Pred. No. 6.7e-36;
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